

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCACTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AACTGTATGCAATGTTTCTGACTCTCGTTTTTTTTGGTTCGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCTTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCTCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCATGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902

><subunit 1 of 1, 245 aa, 1 stop, 1 unknown

><MW: -1, pI: 8.36, NX(S/T): 1

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNYSLLNEKATNVPF  
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-42

#### **Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

#### **N-glycosylation site.**

amino acids 134-138

#### **Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

#### **N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
GGAGTCGCGCCGCGCCGCGCCGCCCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
GCCACAGCCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCCTAGAAGAGGGT  
GTTCCCTCTTTCGGGGGTCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT  
GCGGCTAACAGGGCCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
GGAATAAGCTCTGCAACTTTCTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAATTCC  
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG  
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
CACATAGCCCACCTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC  
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  
GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57



**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGAGGTACCAGATTAGCCCATTTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG  
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGAGAGCAAACCTCTTCCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAAAAAAAAA

**FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGLGGLIKMVHLLVLGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAAGCCCATTTCTGCAGTGGAAATTTTCATGAACTAGCAAGAGGACACCATCTT  
CTTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT  
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG  
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
CTGATCAATAATGCTGGTGTTCGCGCTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA  
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTCCCTTGCA  
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGGTTTCAATGACAGCTTAAG  
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA  
GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAACTGAAAGGCAA  
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG  
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTG  
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCCTGT  
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG  
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTT  
AAGTATCATCTCTTATCTAAATATTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT  
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW  
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF  
NDSLRRDMKAFGVHVSCEPGLFKTNLADPVKVIEWKKLAIWEQLSPDIKQQYGEGYIEKSLD  
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK  
AELANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGGGCGGGCCCCTTGGGCCGTGCCCACCACT  
GTAGTCATGTACCCACCGCCGCCGCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG  
CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCGGCGCTCGTGCTGGAGGAAATGGA  
AGCAACTGTGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT  
GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTTCAAGGCTAGAGGA  
AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAACCAGCAAATCCACCCGTCTTACCAG  
CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCTGTACAGAAGACACAA  
AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGCCCCTGTGGATCCCCGCCCGGAAGGAG  
ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCAGAG  
CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG  
CACACCAGTGTCATCTGAACATATGCCAGAAGGGCGTGATTGACGTCTTCTGCATGCATGGA  
AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGT  
GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAAGGACG  
TGGACGTCAACCTGTTTGGAGGACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC  
CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCC  
CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG  
GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG  
GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG  
TGGGGGAGCTTGCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTTGCCA  
GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCAGGA  
GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG  
TGCACTTCAACCTTTACCCCCAGCCGGGCCGTCCGGACGTGGAGGTCAAGCCAGCAGACAGG  
CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGA  
CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTACGCCGATTACACGGGTCC  
CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCAGCCTAGGGAC  
AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCTCTGCCTATCT  
GGACCCCTGCCATAGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
CTGGGTCTGTGGCATTTCCTCAAGGGCCACGTAGCACCGGCAACCGCAAGTGGCCAGGCT  
CTGAACCTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA  
GGCCGTGAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCTC  
CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA  
GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGTGCAGC  
TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA  
CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC  
CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGGCCCT  
CCAGTGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTGCTCTAACCAGCA

**FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN  
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE  
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT  
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTPVHLNY  
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSEWFGLGLTLIDALDTMWILGLRKEFEEA  
RKWVSKKLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI  
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQMIHGLSGK  
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT  
HLLRHSEPSKLTFFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ  
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG  
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD  
AYVFNTEAHPLPIWTPA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
CGCCTCTCCGCACGATGTTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC  
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG  
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACCCTGTCAGTGCTGGT  
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA  
GCAGGAAGAAGATCCGGCACCAATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC  
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC  
GCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCGCCACCTGCATGACCCAGCCTGGCGG  
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC  
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCCTGTCCG  
GGACCCCCCTGCCTTCTGTCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG  
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCC  
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFSLWLQLSCSGDVARAVR  
GQQQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPPEAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDEFYRRIKGAGLQLFRPSGI  
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310



**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTCAATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT  
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ

PRGEGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGCGGACAAAG  
GAGCATGTCCGCGCCGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG  
GCCCCGCGCCGCTCCTGCCCCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCG  
CTCGCCCCGCAGGCCCGGCCCGCAGCATGGAGCCACCCGGACGCCGGCGGGGCCGCGCGCA  
GCGGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGCG  
GCGGCGGCGCCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC  
AGGGCGGCGGGCGCCGCGGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTT  
GCCCCCAGATACTCTGCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG  
AGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT  
CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCTCTCTAAAAAGATTGGATCT  
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAATCTGGTTC  
GGCTAAACCTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGCG  
TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTGTGTGACTGTAACATACTGTGGAT  
GCATCGCTGGGTAAAGGAGAAGAATCATCAGGTACGGGATACCAGGTGTGTTTATCCTAAGT  
CACTGCAGGCCCAACCACTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCTCCGCTT  
GAATTGCCGCTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT  
TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTTGGTATCAGGATG  
GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAATGATTACAAAC  
TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTACTGGAAATTG  
GGGCTGTCTATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAGGTGACTTCAGATGG  
CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
TTTGGGCAGATGATGATTATTCTCGCTGTCTAGTATGCAAATGATGTCACTAGAGTTCTTTAT  
ATGTTTAAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
TTACACTGTGGAAGCAGCCAACTTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
TTGAAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAGAGCTAGGTGACGTGATGGTT  
GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCCTGTGGCTGGCGCAGAGGGAAGC  
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCTCAAGTCT  
ACTGGCTTCACGGGGATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGG  
ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTTAAGT  
GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
AAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
AAAGATTTTTTTTTGTCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATA  
ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGCCTTTGATTCCCTTT  
CTTCACATAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAATATACT  
ATTGTTACATGTGAAAAAATTTTATTGACTTAAAGTTTATTTATTTGTTTTTTTGCTCCT  
GATTTTAAAGACAATAAGATGTTTTCATGGGCCCTAAAAGTATCATGAGCCTTTGGCACTGC  
GCCTGCCAAGCCTAGTGGAGAAAGTCAACCCTGAGACCAGGTGTTTAAATCAAGCAAGCTGTAT  
ATCAAAATTTTTTGGCAGAAAACACAAATATGTCTATATCTTTTTTTTAAAAAAGTATTTCA  
TTGAAGCAAGCAAAATGAAAGCATTTTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT  
GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACTCCAGCACCCCTAATGGAACCACATT  
TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAAATCTCACAG  
TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCAGTCATTTTAAATGGC  
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA  
TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

**FIGURE 16**

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
VVCSSLELAQVLPPDTLPNRTVTLILSNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT  
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF  
SHRQVVFEQDSLPPFQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT  
ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDWRWPRTLGIT  
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL  
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKEKLGDMVDIASNIMLA  
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
433-437, 453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
384-390, 403-409, 554-560

**FIGURE 17**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA  
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

## FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

Signal peptide:  
amino acids 1-21

**FIGURE 19**

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTT  
CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC  
GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG  
CCTGGGGTCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC  
CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
GGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTGCTTCTCCGTGACCCTGATCA  
TCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGCGCAACTTCCCC  
ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
CTATGTCCAGTTCCTGTCCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCGGCAG  
ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG  
CATCATCTTCGCGTTTATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
GAGTGCACCAACGTGCTACCCATCCCCCTTCCCCAGCTTCCTGTGCGGGGCTGGCCTTGCTGTC  
TGTCCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG  
GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT  
GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
TGACCTGGTGCACTCTGCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC  
CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
TCCGCTTTTCTGTCTTTTCTTCTTCTTCTCCCCCTCCCTCCACCTTTTTCTTTCTTCTCC  
CAATTCCTTGCACTCTAACCAGTTCCTTGGATGCATCTTCTTCTTCCCTTTCTTCTTGCTGT  
TTCCTTCTGTGTTGTTTGTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTTT  
CTTTTCTTTCTTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
TGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTCAAGCGATTCTCCTCC  
CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT  
TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCTGTGCGGCTTTCTTATCTGCCTGT  
TTTGCAAGCACCTTCTCCTGTGTCCTTGGGAGCCCTGAGACTTCTTTCTCTCCTTGCCCTCA  
CCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCCATGCCACAGCCCC  
CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
GTGTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGGCCCTCTTTCT  
CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATAT  
ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG  
CCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTTCATCCCAACTATTCT  
CTGTGGTATGAAAAAG

**FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727  
<subunit 1 of 1, 322 aa, 1 stop  
<MW: 35274, pI: 8.57, NX(S/T): 1  
MPVTVTRTTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG  
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY  
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI  
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPIPFPSFLSGLALLSV  
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD  
LVHSAHLVFKV

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21



[illegible]

**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHMDPNYCHPSTSLHLCS  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY  
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSSSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT  
GGCACCCCTCCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTTCTAATGCACGA  
CAGATTCCTTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TAAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA  
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCACATCTACCATTTCACACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTCACTTGCTCTTTGGTCAATGACACCGTGAAAACCTCTGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAAATTACCAATAATTCAAACTCTTTCCAA  
ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTTCGGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTTGGGCTACTTGTTGTGTGGAAAAAGGAAAAC  
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT  
GATTACGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCCTATGGATGACATACC  
TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCTCTA  
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT  
TCACCATTACAGCCCTGCCTCATAACTAAATAAAAAATTATTCCACCAAAAAATTCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

**FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA  
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSGNSSYYNPTLND  
SA  
MPSEENARDGIPMDDIPPLRTSV

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

**FIGURE 25**

AACAGGATCTCCTCTTGCACTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
AGCCCGAAGATTCACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
CTTAGGCCTTTCATTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA  
AATTCCTTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG  
CAATTATTTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAACTGC  
TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGGTCCTTGG  
CAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG  
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
AAGTCCTTCCGCCTTCGTGCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA  
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT  
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
AAAAAAAGGAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAAT  
TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAG  
GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC  
GTTGTTTTTTTTGTTTGTGTTTTTTCTTTTCTTTAAGTAAGCTCTTATTTCATCTTATG  
GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTGAACCTTTTGTGTAAAATATA  
TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA  
AATTACATCTTTCAGATTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG  
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA  
CCCTATAATAAATTTTACTCTATACAAAAA

**FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF  
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA  
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLAGS  
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR  
HFPNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCCAGTCCTGTACGCC  
AAGGAACTGGTCCTGGGGGCACCAATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCGCTCTGTGCCCCCTGAAGGCCACGTT  
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG  
GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA  
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
CGACAGCAGGCCCGAGGAAGCCCTGGATTCTTCCCGGCAGCTCCAGGCCGACATCTTGCCG  
CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG  
AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCCAG  
GAAGCCAGGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGACAGAGTGTCCACCCCAG  
TGTCTTAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTGCGGGCCCCCAAGTGGTCACCTCCCC  
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTTGACACTCCCTCCTTGGCCTCCCTGTGG  
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA  
GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCTGAAGG  
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
GATCAGGTTGAATGAATGGAACCTTCTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
TGTCACAATATTTCGTCACTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
CTGGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCCAACCTCTGCACAGCTCT  
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA  
AAGA

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLLLLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP  
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248



**FIGURE 29**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA  
GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG  
GCAAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATG  
AAGTTCCAGGGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG  
CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC  
TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCT  
GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG  
GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG  
CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA  
GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG  
AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG  
GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT  
CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC  
TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT  
GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC  
TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG  
TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTGG  
GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCCTGGGGA  
TCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACC  
CGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGAGCGGGGAATCTGGGATTGAGGGCTTCA  
GAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGG  
GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT  
TGGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACCTTTGACACTTTCT  
GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA  
AGCTCTCGCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT  
CCCTCCTTAAACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTA  
GCTGCCCCACAA  
AAA

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
```

```
><subunit 1 of 1, 440 aa, 1 stop
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><MW: 42208, pI: 6.36, NX(S/T): 1

[illegible]

**Signal peptide:**

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

**FIGURE 31**

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG  
TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA  
CTCTCCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGTCGAGGAGAGTGAGGGGAAGATGTGTTTCTGGAACAAGC  
TGCTGCTACTTGTCTGCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTCTTTCTGGAAGAGG  
GTCCCTCATATGCCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGGACCAGC  
AGTGCTCTACACCTGTGCCCCCTACATCGGAGAGCTCCGGAAGTGTCTCGCTTCTGTTGGGTGTCAGGCAGTAGTG  
GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCAACAGCCTGGGAGCCAGCCTTCCAGACCA  
GCCAGGGGCTGCAGGCACAGCTCGCCAGGCCTTTTCCACAACCAGCCGCCCTCCTTGCGCCGGACCGTAGAGT  
TCGTGGCAGAAAGAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCGCCAGG  
CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCAGCTGTTGGAGATCT  
TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCGTCAAAGGAAGAGCCCTG  
GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC  
TTGCAACAGAGAAAAGCCTGTGCTTGGCTGTGAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
TGAGTGCACACTTCGAGCCAGGGTCTGAACCTGTGCCCCGGGGGGAGCGGAGGGGCTGCTCCCGCGCCTGAC  
GTGCTCTCCTTGGCCGTGGGGCCACGGGACCCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC  
CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGTCTGTG  
GAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCTTATCTTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG  
CAGGCTCGAAGGCTTCTGCACATGCTGCTTTCTTGTGGAAGGAAGACTTTTCAGGGGCGGGTTCGCTGCAGCTG  
CTGCTGAGCCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGTGCTATTCTTGCTA  
CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCTGCCTGGGCAGCCTCCACCAGGCCAG  
TGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACC  
CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC  
CTGCCCTTGGGCATTGCACCAGAACCCTGGACCCCCGCTCACGAGGAGGCCCAAGTGGCCATGCAGACCCTCAC  
TGTTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCCCTGGCATCCCACCACGCGA  
ATCCTAGAGGAAGGAGAGTTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTGGAGTAGAA  
GAGGTGGTGTGTTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAGCCCT  
CATTTGCTATCCCAGCATCTCTTAAACTTTGTAGTCTTGGAAATTCATGACAGAGGCAATGACTCCTGCTTAAC  
TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT  
ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCGTGAATCCAGCACTTTGAGAGGCTGAGGTGCGCG  
GACTGCCCTGAGGTGAGGAATCAAGACCAGCCTGGCCAACATGGCAAAACCCCATCTCTACTAAAAATAAAAAA  
TTATTAGCTGGGCATGGTGGTGTGTGCTGTAAATCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC  
CTGGAGGTGGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTAACAGAGCGGAGACTTTCTAG  
AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCCTG  
TGAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGCTTTTGAATAAA  
CTGGTTTCTTTAAAAAAGGGCTTTTATTAATAATCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC  
TTTTTTTTTTTTTTTTTAAAAAGGGCTTTTATTAATAATCTCCCCACACGATGGCTCCTGCAATCTGCCACAGCTC  
TGGGCGGTGCTCTGTAGGGAAGGCCCTGTTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG  
GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTCCGGGACACAGAGCTGCGGGGTCTGGGGGCACCGGG  
AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTG  
GGTCCACCCTGAGTGGCACGGGAGCAGCTGTGGCCGCTGCTCTCYTAGGCCAGTCTGGGGAAACTAAGCTC  
GGGCCCTTCTTTGCAAAGACCGAGGATGGGGTGGGTGTGGGGGACTCATGGGGAATGGCCTGAGGAGCTACGTGT  
GAAGAGGGCGCCGGTTTGTGGCTGCAGCGGCCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTCCGTCTA  
ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTTGGACGAGCGTCAT  
GTTATTTTCACAACTGTCTCGACGTTGGCCTGGGCACGTGATGGAATGGCCATGTCCCTCTGCTGCGTGGAC  
GTCGCGGTGCGGAGTGCAGCAGCCAGAGCGGGGACAGCTGCGCCTGGGGGTGAGGGGAGGCGCCCCGGGAGGG  
CCTCACAGGAAGTTGGGCTCCCGCACCAACAGGCAGGGCGGGCTCCCGCCGCGCCGCCACCACCGTCCAGG  
GGCCGGTAGACAAAGTGAAGTGCAGCTTGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGAGTGGCGCAGCGCG  
TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCAGAACAGCCGGTGCCT

**FIGURE 32**

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

### FIGURE 33

33/270

**FIGURE 34**

MSSNKEQRS AVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVVHVG MVPPNYCSQRPR LQRMPYH  
YYEPKGPDECVTYIQNEHSRKG NHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

**FIGURE 35**

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT  
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCGAGGTGCTGAGGGGCTGG  
GGCAAAGGTGAAAGAGTTTCAGAAACAAGCTTCCTGGAAACCCATGACCCATGAAGTCTTGTGACATTTATACCGT  
CTGAGGGTAGCAGCTCGAAACTAGAGAAGTGGAGTGTGTCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC  
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
AGGCCTGAGGTACACTGGCTTGCCTCCTCCTAGCCACAGCAGGCTGCTTGTGACTTGAACGAGGTCCCTCAG  
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCA  
AGGATGAATGTAACCTGGCGCCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCCTCATCACC  
CACGGGACCCCTCGTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCCTGCG  
GGGCTGTGGCCAGCGTCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGACGACGCTG  
ATTGAAGTGGATGAGGGAACACAGCAGTCAATTGCCCTGCCACCTGCCTGAGAGCCACCCCAAGCCAGGTCCGG  
TACAGCGTCAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGATT  
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAACACC  
TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCCAGAGGCC  
CAAACCATCATCGTACCAAAGGCCAGAGTCTCATTTGAGAGTGTGTGGCCAGTGAATCCCACCCCCACGGGTC  
ACCTGGGCCAAGGATGGGTCCAGTGTACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC  
ACCACGAGCGAGGAGCTCAGGCACCTACCGCTGACATGGCCAGCAATGGGGTTGGGACGCCCCGGGACGCGT  
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCGATGGAGCTATCCAGCTGGTTCATCCCTGGGGC  
CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCCC  
CTCATCTCCAGCCAGCGCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTCTCAGCATGGGGCTGAGGACGAAGGC  
GTCTACCAAGTGCATGGCCGAGAAGGAGTGGGAGCGCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC  
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAACCTCGGCAAC  
CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCAACGTCAGTGGGGCTGCTTCCCCGAAGTGT  
CCAGGAGAGAAGGGGACGGGGCTCCCGCCGAGGCTCCCATCATCCTCAGCTCGCCCCGACCTCCAAGACAGAC  
TCATATGAACCTGGTGTGGCGGCCTCGGCATGAGGGCAGTGGCCGGGCGCCAACTCTACTATGTGGTGAACAC  
CGCAAGCAGGTACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAACGACACCGCCTGACCTC  
ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACCTGTGCGGGAGAGGGCCAGACAGCC  
ATGGTCACCTTCCGAACCTGGACGGCGGCCCAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC  
GACCCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCACGGCCGCTCTCCCCCAGAAGCTCCCGACAGG  
CCCACCATCTCCAGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCTCAATC  
CAGTCCCTTCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCCAGCGCCATCCCCCA  
TCGCGGCTGTCCGTGGAGATCACGGGCCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG  
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGGCTACAGCGGTGCGGTGTACGAGAGG  
CCCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC  
CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGAGCTGACATGATGAT  
GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCTAC  
GACATTAAGATGCAGTGTCTCAATGAAGGAGGGGAGAGCGAGTTCAGCAACGTGATGATCTGTGAGACCAAGCT  
CGGAAGTCTTCTGGCCAGCCTGGTTCGACTGCCACCCCAACTCTGGCCCCACCACAGCCGCCCCCTTCTGAAACC  
ATAGAGCGGCGCGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTGTC  
CTGGGCTCCATCGTTCTCATCATCGTCACCTTCATCCCCCTTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAACAT  
ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCACCCCTCCTGCCCCGTATACTATGGTGCCATTGGGAGGACTC  
CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGCATGAAGCCCAGCAGCACTGCCAGGCGAGCTTCAG  
CAGCAGATGACACCAGCAGCCTGCTGAGGCAGACCATCTTGGCAATGGATATGACCCCAAGTCAACGATC  
ACGAGGGGTCCCAAGTCTAGCCCCGACGAGGGCTTTCTTATACACACTGCCCGACGACTCCACTCACCAGCTG  
CTGCAGCCCCATCAGACTGCTGCCAACGCCAGGAGCAGCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC  
CCCGACAGTCTGTCTGGAAGCAGTGTGGGACCTCCATTTCACTCAGGGCCCCCATGCTGCTTGGGCCCTTGTG  
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAGTGGAGGAGACTGGTGTCCCCAGCACCCGCTAGGG  
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCCACTGGTGCCTGTGCTTTTGAACACCCACCT  
CTCACAATTAGGCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAAAAA  
AGAGACAGAGAAAATTGGTATTTATTTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAATAAATGTA  
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTTACCCGTTGAGGTTGGAGAGGGAAAAATAAGAAGCTGCCA  
CCTAACAGGAGTCAACCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCTCTGCAGTG  
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCTCATCAGAGCA  
TGAGGGAACAGCAAGGGGCACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAA  
ACATTTTCTAAGATGCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAAAACCTTCCAGAAAT  
CAATAATCCGTGGCAACATATCTCTGTAAAAACAAACACTGTAACCTTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

**FIGURE 36**

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP  
RMNVTWRLNGKELNGSDDALGVLI THGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
ANLQDFKLDVQHVIEWDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
IVNASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTI IIVTKGQSL  
ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
RRALRVLSMGPEDEGVYQCMANEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKQGAPAEAPI ILSRPRTSKTDSYELVWRPR  
HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASQSSSQPDHGRLSPPEAPDRPTISTASE  
TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV  
RALNMLGESEPSAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMI PASNNNT  
PIHGFYIYYRPTDSDNDSYKKDMVEGDKYWH SISHLQ PETS YDIKMQCFNEGGESEFSNVM  
ICETKARKSSGQPGR LPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL  
IIVTFIPFCLWRAWSKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK  
SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
PPCCLGLVPVEEVDS PDSCQVSGGDWCPQHVPV GAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879



**FIGURE 37**

CGGGAGGCTGGGTCGTGATCCGGACCCATTGTGGCCTCTGCCCATCGCCTGCTCCTC  
CCAGGCTCCCGCGGCCGACCCCCGCGCAACATGCAGCCCACGGGCCGCGAGGGTTCCCGCGC  
GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC  
AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
CACCCCCAAAACCCTGGACCTTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
TGGACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
GTTAACCTGCGAAATTTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT  
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC  
CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG  
AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGCCATCGTGATGGTGACACT  
GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTATGACGGGACT  
GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCAGTCCTGATAGAGGAGTTGCT  
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT  
TCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC  
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT  
CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC  
TGCTGACCACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

## **FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVPS  
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ  
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS  
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT  
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL  
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV  
STYPVLIIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFPYGQLSTSCH  
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGCCATG  
AAGCTCTTATCTTTGGTGGCTGTGGTCCGGTGTGTTGCTGGTGCCCCAGCTGAAGCCAACAA  
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
GTGCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
CACCACCACCATCAAGGTCATCATTGTCACTCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC  
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTTAGATGGGCTGG  
TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTCTTCTCCTT  
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA  
ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTCTTCA  
GGAAGTCAAGTGTCTGGGAGGAAAGCATGGCCCAGCATTAGCATGTGTTCCCTTTCTGCAGTG  
GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCAGTGA  
AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTG  
CACAGTCACTGAGCCAGACGGTCCGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
CACCACAGCCCCTGTACTTGGGTGCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA  
GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG  
TTTTATTTCTCTCA

**FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM

PVPGHDVEAYCLLCECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE

QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

ACGCGGCTCTCGCTTGGGTTTCCGCTAATTTCTGTCTCTGAGCGCTGAGACTGAGTTTCATAGGGTCCTGGGTCCCCGA  
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCAGCCCAAGTGAGGGGCCCCGTGTTGGGGTCTCTCC  
TCCCTTTGCATTCCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATAGGCCCGCGTTGATG  
CGGAGCAAGGATTTCGTCTCTGCTGCCCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
TCGCGGGGCCAAACTCAACTCCATCAAGTCCTCTCTGGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG  
GGCATGTACCAAGGACTGGCATTTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCCTACCCTTTGTAGCAGT  
GATAAGGAGCTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCCTGCATGTGTGTGTCGGAGA  
AAAAAGAGCGCTGCCACCGAGATGGCATGTGTCTGCCCACTACCCGCTGCAATAATGGCATCTGTATCCCAGTT  
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC  
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA  
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA  
CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAACAACGCAAGAAGGGTTTCTCATGGGCTGGAAATTTTCAGCGT  
TGCGACTGTGCGAAGGGCCTGTCTTGCAAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
TGTGAGAAAATTTGAATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTATATGCAATTATAG  
CATGGTGGAATAATGAAGTTTCAGATGCAGAGAATGGCTAAATAAGAAACGTGATAAGAATATATAGATGATCACAA  
AAAGGTGAGAAAGAAACATGAACCTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTCTTCCATTATG  
CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAATTT  
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTTCAGATTGCTGATTGC  
TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAAATTGTGTA  
TACAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAATGAAAACATGGGACATTGTTAATTTACAACAGAAAAT  
TACCTTTTGATTTGTGAACACTACTTCTGCTGTTTCAATCAAGAGTCTTGGTAGATAAGAAAAATCAGTCAATAT  
TTCCAAATAATTGTCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAATAAATAACAAACAAACAG  
CCACAATACTTTTTTTTTTCAAATTTTAGTTTTTACCTGTAATTAATAAGAACTGATAACAAGACAAAAACAGTTCC  
TTCAGATTCTACGGAATGACAGTATATCTCTCTTATCCTATGTGATTCTCTGCTCTGAATGCATTATATTTTCCA  
AACTATACCCATAAATTGTGACTAGTAAAATACTTACACAGAGCAGAATTTTTCAGATGGCAAAAAAATTTAAA  
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT  
GATAGAATTAGATTGGTAAATACATGTATTATACATACTCTGTGGTAATGAGACTTTAAGCTGGATCTGTACTG  
CACTGGGAGTAAGCAAGAAAATTTGGGAAAATTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGTCTG  
AGGCACAAGTTGGCTGTTTACTCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGCTAT  
CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCCGTACTATCCTCAAATATTTATTTTATAG  
TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTTCAAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG  
TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCAAACCTCTGCAGCATCTG  
CTTTATTGCCAAAGGGCTAGTTTTCGGTTTTCTGCGAGCCATTGCGGTTAAAAAATATAAGTAGGATAAATTGTAAA  
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTTGAACCACTTTTACTACTTTTTTTAAACTTT  
AACTCAGTTCTAAATACTTTGTCTGGAGCAAAAACAATAAAGGCTATCTTATAGTCTGACTTTTAAACTTTTTG  
TAGACCACAATTTACTTTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG  
AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCAACTTCCCACATATATTTACTAAGATGATTAAGACTTA  
CATTTTTCTGCACAGGTCTGCAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAGTTTGTATAAACAGGT  
TGCTATAAGCTTGTGAAATGAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATTTTACAAT  
TTGGTTTTCTGCAATATTTTTCTTATGTCCACCCTTTTTAAAAATTTATTTTGAAGTAATTTATTTACAGGAAATG  
TTAATGAGATGTATTTTCTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC  
TTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAATTTTTTCTCCTCTAAAAACTGAAAAAATAA  
AAAAAATAAATAAATAAATAA

## **FIGURE 42**

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRC  
NN  
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA  
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT  
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG  
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT  
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA  
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAATACTACTTCTTGGGACCTCAAGCC  
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCCTCCT  
CCTGGTTTGGAGTCCTTTCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG  
TCCACCAGCCACAGCCCAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
ATCCCAGCTTCTGCAGTGGAATGCCTGGTTTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
AAAATAGTAATCAGATTCCCATCAGCTTGTATTCTGAAGTCTTTAAGTGAGCCTTTGAATACA  
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACTTCCGTCATTACCTCCTG  
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC  
AGAGTTCTGTGCATAACAGGATCCCATAACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
GGAACCATCATGAATGGACATGGTGGTGGTCTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
CAGCAAGCTACTCTTGTCTATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA  
TGTGGAAAACACCAGTTGGTCAATGGCTCATTCTGTTAAAAAGCAGCCCTTTTGCTTTTTTGT  
TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAACAGTATGCAT  
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC  
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAACTC  
TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG  
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
GTCTGAAAAGA

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP  
PGLESFPSQAKLRESTPGDSPSTVKNLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**  
amino acids 1-24



**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTGCT  
TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA  
GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT  
GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG  
GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA  
CGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCCGACGAGGGCACCTACTCCTGCCACCTGCAC  
CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC  
GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG  
ACCCACACTGGCGCGCGGCCACAACGTCAATGTATCGTCCCCGAGAGCCGAGCCAC  
TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC  
TGTCTCCTGGCCGCCCCGAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA  
AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT  
TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTCCGGAAGGAGAACT  
GCAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT  
GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
AGCATAGCCCCCACCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAAC  
AAAATCCCCTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG  
AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAAGTGGGGTCAGCCTCA  
GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
CTTTGGGGCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG  
CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT  
GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA  
CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT  
GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTTAAAAA  
AAAAA

**FIGURE 46**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT  
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRHVEEAQQVVHWRQPPGVPHDRADRLDL  
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF  
HLTVAEPHAEPPIRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL  
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN  
NILKERAELAHSPLPAKYIDLDKGFRKENCK

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTT  
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT  
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT  
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC  
CGTGTCTTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTCGGGTCACCATTTGTCTGCATGGTGATCC  
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCTATG  
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGG  
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
AGGTACTACATGAGGCCTGTTCTTTCGGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA  
GGACTCCCTCAGTGCCCTTCGGTGGCCTCCAGATTCAATTGATTCCACACACCCCCCTCTCC  
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC  
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACTTTGCTGACCTAT  
GTGGCCGGCAGCTCACC GCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG  
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGT  
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG  
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  
CTCAGCCTGCTCTACCCCTCCTGGTGCACCTCATCTAGAAAGGGAGGACACAAGGACATTGGTG  
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC  
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
GTGAGCCACGTCCATGCCCATTCCGTGCAAGGCAGATATTCAGTCATATTAACAGAACACT  
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA  
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCAGCT  
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA  
AGTCCCCCTGGCATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
GCGGGTGAACAACTGCCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCATGAAT  
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGCCTGGG  
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
GTATTCAAAAA

**FIGURE 48**

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFFSLGI  
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY  
LLLSRLEYARYYMRPVLA AHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIP LFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472

**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA  
TCTCCCACCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCC  
TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC  
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT  
GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC  
TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG  
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC  
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCGTCCCAGGAAAAGGGCCACTCGCCCGAAGA  
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC  
CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
CGCCGAGGCCCTCCGGGCCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG  
CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG  
CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCGCGAGGCCCTTCTGGCGCGAGGA  
GCACATTGAAGGCGGCCACTCAAAACACCGATCGCCCGTCCGCGCATGATTTTCTACCCGCCGC  
CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCCGACGCGGCGGCAGCGTTCCGC  
GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGTCGTCAAGCGTTGGGCGGAGGACCAGCACA  
GCCAGGGTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT  
CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG  
GTGGCCAGCAGCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG  
CCAGTTATCTCTCAAAAACAGACCCACACGAGGACCTCGCATTAAAGTATTTTCGGAAAAA  
AA

**FIGURE 50**

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKLGALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
KVLKADVLLTASGPAVKRITFSPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGTGGGGACACTCTGGGCCGGCCTTCTG  
CCTGCATGGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGAC  
TCGTGTGGCAGGAAGAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCC  
CTCGCAGGGTCTGAATTTCTGTCTGTTCACAAAGATGCTTTTATCTTTAACTTTTGTTCCTCC  
CACTTCCGACCCCGGCGTTGATCTGCATCCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACC  
AGACCTCAACCCGTCTTACCTCTTCTTGACCTGAACAATCAGTCTGTGGGAATTGAGGGAGGAGCAG  
GAAGGGGGTTTCCCAGAAGAACAATGACCTAACAAGTTGCTGCTTCTCAGATGCCAAGACTATGTATG  
AGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTGCTTGGGATATAGAAAACCAAACCAG  
CCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTCTGTCTCTTGCA  
TAAAGGTTATAAATCATCACCAGACCAGTTTGTCTGGCATCTTTGCTCAGAATAGGCCAGAGTGGATCA  
TCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAA  
GCCATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAGGCATT  
GGTGCTGATAGGGAATGTAGAGAAAGGCTTACCCCGAGCCTGAAGGTGATCATCTTATGGACCCCT  
TTGATGATGACCTGAAGCAAAGAGGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAG  
AACCTAGGCAAGTCATCTTTGCAAAACCTTGCCCTGCTTACCCAGAGAAGACCTGAGCGTCTATCTGCTT  
CACCAGTGGGACCACAGGTGACCCCAAAGGAGCCATGATAACCCATCAAAATATTGTTTCAAATGCTG  
CTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCCCACTCCTGATGATGTGGCCATATCCTACCTC  
CCTCTGGCTCATATGTTTGGAGGATTGTACAGGCTGTTGTGTACAGCTGTGGAGCCAGAGTTGGATT  
CTTCCAAGGGATATTGGTTGCTGGCTGACGACATGAAGACTTTGAAGCCACATGTTTCCCGCGG  
TGCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCTGAAGAAGTTC  
TTGTTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAGTTT  
CTGGGACAAGCTCATCTTTGCAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACTG  
GAGCTGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAGGTGTATGAA  
GCTTATGGTCAAACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTCA  
CGTTGGGGTGCCCCCTGGCTTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACCTACTTTACAG  
TGAATAATGAAGGAGAGGTCTGCATCAAGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAG  
AAGACACAGGAAGCCCTGGACAGTGATGGCTGGCTTACACAGGAGACATTGGTCTGGCTCCCGAA  
TGGAACTCTGAAGATCATCGACCGTAAAAAGAACATTTTCAAGCTGGCCCAAGGAGAATACATTGCAC  
CAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTTACAAATTTTGTACACGGGGAGAGC  
TTACGGTCATCCTTAGTAGGAGTGGTGGTTCTTGACACAGATGTACTTCCCTCATTTGCAGCCAAGCT  
TGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTTAGAAGACT  
TGCAGAAAATTTGGGAAAGAAAGTGGCCTTAAACTTTTGAACAGGTCAAAGCCATTTTCTTTCATCCA  
GAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTTCCAA  
ATACTTTCGACCCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAAGTACC  
TGCCGGCCCACTGTGCACTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTGCCTTT  
CCTCCTATTTTCTTAACTGTTAAACTCTAAAGCCATAGCTTTTGTCTTATATTGAGACATATAAT  
GTGTAAACTTAGTTCCCAAATAAATCAATCCTGTCTTCCCATCTTCGATGTTGCTAATATTAAGGCT  
TCAGGGCTACTTTTATCAACATGCCTGTCTTCAAGATCCAGTTTATGTTCTGTGCTCTCCTCATGA  
TTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGTCAAAGGGACCCTCTGTGCCTTCTTCTT  
TGTTTTGTGATAAACATAAATTGCCAACAGTCTCTATGCTTATTTACATCTTCTACTGTTCAAACATA  
GAGATTTTAAATTCTGAAAACCTGCTTACAATTCATGTTTCTAGCCACTCCACAAACCACTAAAAT  
TTTAGTTTATAGCTTACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTTCTGCGT  
AAATTAATTTGTGTACTGAAGGGAAAAGTTTGATCATACCAAACATTTCTAAACTCTCTAGTTAGAT  
ATCTGACTTGGGAGTATTAATAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGC  
ATTATTTACAGTAGGAAGTGGGGAGTAAATCTGTTCCCTACAGTTTGTCTGCTGAGCTGGAAGCTGTGG  
GGGAAGGAGTTGACAGGTGGGCCCAGTGAACCTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCT  
CCTGAACTGGGAACAAAGATCTACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGG  
AACCAACTGATCTCCCCACCCTTGATTAGAGTTCCTGCTCTACCTTACCCACAGATAACACATGTT  
GTTTCTACTTGTAATGTAAAGTCTTTAAATAAACTATTACAGATAAAAAA

**FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775  
<subunit 1 of 1, 739 aa, 1 stop  
<MW: 82263, pI: 7.55, NX(S/T): 3  
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN  
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTS  
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYQVSDRAEYLGSCLLHKGYKSS  
PDQFVGIFAQNRPEWIISELACYTYSMAVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL  
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFKLCVEHAYEPTPDDVAISYLPLAHMFERIVQ  
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGRRVRIVTGAAPMSTSVMTFFRAAMGCQVY  
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
GYLKDPEKTQEALDSGWLHTGDI GRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR  
SQPVLQIFVHGESLRSSLVGVVVPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI  
GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622



**FIGURE 53**

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG  
CCCCGGGGCCCCCTAAGCCATTCTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
CCGGTATGGACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
GACAGGGGCGCGTGCTTTTCCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA  
CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA  
GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG  
AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGCCACGTG  
ATGGCAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCT  
CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC  
TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC  
TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC  
TAAGTCACCTGCCCTCTCTTCTGGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA  
GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCGCGCGC  
TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
GTTTCAGCCCTGACCCACTCCAGACAACAAGTCTCAATGTGCCTGTGGCTGTCAATTGCAG  
GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCT  
CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC  
ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT  
CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCAGTTTCTGAGCCAATCCATCCACCT  
ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA  
CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA  
TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG  
TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTCACGAGGCC  
TACTTCAAGAAGCACAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
GAAGAAAGAAGCTTATGAAGTGGAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
TTTATTCTGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA  
TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA  
ACCACTTCTGGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC  
ACCCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
ATGAGACCTCCTCCAGGACCCCTGCGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA  
TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCGTTTCTGAGTT  
AAAAGTCTATTTATTTACTTCTTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG  
ATCCCTAGCAGCTCATCCTGCCCTTTGAATAACCTCACTTTCAGGCCTGGCTCAGAATCTA  
ACCTATTTATTGACTGTCTGAGGGCCTTGAAAAAGGCCGAACCTGGAGGGCCTGGATTTT  
TTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC  
CAACCCATGGACAGGCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCTTA  
GACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTGTCCAGATTTCCAAGCTGGATAAGTT  
GGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185  
><subunit 1 of 1, 660 aa, 1 stop  
><MW: 75220, pI: 6.76, NX(S/T): 0  
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTVIVNIKLILDTR  
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
REQGRGIHVIVLNQATGHVMAKRVDFTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK  
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS  
AEEAECHWADTELNRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN  
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPEMDVVALFGLRGIQHTPISIKNARVSQHY  
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA  
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMMRMPEQRRGRECIIPDVS  
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKKKEAYEVEVHRLLEAEVLDHS  
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLDVIRGNHRGLWRLFRKKNH  
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features of the protein:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC  
CTGTTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA  
AAGGAGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA  
CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG  
GTGCTGGCCTTCTCTGTGGAACGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA  
GATATTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC  
AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCTATATTGGTG  
TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGGTAACCTCCCATGTGCATTCT  
ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAATCACCACCACGCTGGGTCTGGTTGTCCA  
TGCTGCAGCTGATGGTGTTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT  
GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT  
GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG  
CCATGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCTGAGGTGGGCGGA  
ATAGGGCACAGCCACAAGCCCGATGCCACGGGAGGGAGAGGCCCTCAGCCGCTGGAAGTGGCAGCCCT  
GGTCTGGGTTGCCTCATCCCTCTCATCTGTGCTAGGACACCAGCATTAAATGTTCAAGGTCCAGC  
CTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCAGCTGACAGCTACTCACTTCTCAGTC  
TCTTGTCTCACCTTGCGCATCTCTACATGATTCTTAGAGTCCAGAGGGGAGGTGAGGTAAACCTG  
AGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTG  
TATCTTTTAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAACCTATTCTCAGGGAAGATG  
GAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT  
GTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT  
AACATGGTTCCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA  
GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT  
TAAACAGCTCCTTTGGCAGTGCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG  
TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAAT  
ACCTGTCTCCACATTCCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA  
CAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAAATTTTAAGTGATTTTGGATGGTTAT  
TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAATGTATGGTTGTCTTTTTTTTTTTGTTTT  
TTTTTTTTTAATTAATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT  
GGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAAGTGTGTCCTA  
TTGATTTAAAGCTTATGGAATCATGTCTCTGTCTCTTCGTCTTTTCTTTGCTTTTCTTCTAACTTT  
TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTTGTGTGGGATGAATT  
CTTATCAGGACAACCACTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATTCTTTATCCCTT  
CAAAGAAATTACCTTTGTGTCAAATGCCGCTTGTGAGCCCTTAAATAACCACTCCTCATGTGTAA  
ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAGTGTTTAAACAGACTAGGATA  
ATTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTTGTCAAATAAGTGATAAATATTGTAT  
TATTAATTTATTTTACTTTCTATACCATTTCAAAACACATTACACTAAGGGGGAACCAAGACTAGTT  
TCTTCAGGGCAGTGGACGTAGTAGTTTGTA AAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG  
ATTTATTTCTTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCT  
GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA  
ATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT  
GACTGGTGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACTATATGGTTGCCTAGATTCTCTCTGGA  
AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAAA

**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVMHEHEHSHDHTQLHAYIGVSLVLGFVFMLLDQ  
IGNSHVHSTDDPEAARSSNSKIITTLGLVVHAAADGVALGAAASTSQTTSVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

**FIGURE 57**

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
ATCGTCTTGCGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT  
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGA  
AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
CACAACCTTCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA  
TAACATCACACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAAGAACAGACCAACCTGGAG  
AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA  
GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGT CAGTGAGCCAGGAAAATCCAGAGA  
TGGAGGGCCCTGAGCGAGACCAGCTTGT CATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
AATCATACACTCTGAATTGAACTGGAATCACATATTTCACAACAGGGCCGAAGAGATGACTA  
TAAAATGTT CATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

**FIGURE 58**

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQODVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

**FIGURE 59**

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA  
CCAGTGGCTTCTGCTCAACCGTTTGGAGCTCAACACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC  
TGCCATGGGGGAGCCAAGGGAACCTGGGGCTGCTGGATGGCTTCCCGATTTTCGCGGGTGTGTTGGTGTGA  
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACAGTGCCTAGAGAGCTCCTGTCTCCCTACCCT  
TCCTGGGCAAACTAAGCTCCTTGCAGAGGATCCCTGGAGATTAGCCCCACCATGCCCGGCTCTACCGATCTCAGG  
TTGACCTCTACCACCACCATGCAGCGCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG  
GTAGTAACCTCGCCAGCCAGCCATAGTGGAAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGCGTGTAG  
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGTCTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA  
ATGTAGAGACCTAGACACAGTGGACAATGGCATCCTGGAAACACCTCTACCCACCATGGACAGTGGTGAATGGG  
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGCCA  
AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG  
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGTGTCTCTTTC  
TGTATAGCCCCACAGCAGTCTTCCCGAGCACCACCCAGAGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC  
CCACGTGGCCCTGCTGGCTGGGCTGGCCATCCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG  
GGGGTGGAGACTCCAGCCCCACTCCTGTCTTAGCCCCAAGCCTCAGCTCTCATCTCAATGCTCAGCAGGTGT  
CCCCGATTTCTTACATCTACTCAGTGTCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  
TCTCCAAGGCCTCTGCTGACTACAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCTGGTGA  
TTGCTGAGTGCAGCAGTTCCTGCGGGGAGCTCGGGCATGTGCATCAGTCTTGGGCTCGTTTCTCTCTGGTCC  
GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC  
CAGGCTTTCCATTCTGCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC  
TCCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT  
TTCTGTGGAAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTTGGCAACCTGTTCCTATCCCTGGGCCCGTCC  
TGTTACTCCTGCTGTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTTGTTGTAGCTGAGGCCAGGGCCACCCCT  
TCCTTTTGGGCTCATTCACTCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC  
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAAACCCCCACGGCACAAATGGTGCATATGCTAGGCTTG  
GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGGCACT  
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCGAGCCAAGAAATTTATGGTATGGAGCTTGTGTGG  
CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCGGCTATGGTAATCTCAAGAGCCCCGAGCCAC  
CCATGCTCTTTGTGCGCTGGGGACTGCCCCAATGGCATTGGGTACTGCTGCCCTACTGGGCATTGGCGTGGGGG  
CAGATGAGGCTCCCCCGCTCTCCGGGTCTGCTGCTCTGGGGCATCCATGGTGTGCTCCTCGGGCTGTAGCAGGGC  
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA  
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA  
TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAAATCTCAGGGTCCCCTGACTGTGGCTG  
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTGTTGGCCTTCCCACTTCTGCTGT  
TGATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCCCTCTCCTACATCTGCTTGTCTG  
CTGGGATACCCGTCAACACCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA  
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC  
CAGAGGGTCACTGGCTCCTGTACTTGGCTGCTGCTTGTCTAGTGGGAGCCAACACCTTTGCCTCCCACTCTCTCT  
TTGCAGTAGGTTGCCCCACTGCTCCTGCTCTGGCCTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC  
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG  
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTAGATTCT  
TGGCCTGTGCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAGTGTGCCCCCTAAGTTCAATAT  
TTGAGGCTGTGGGCTTCAATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTGGTGATGAGAGTGGATGGTG  
CTGTGAGCTCCTGGTTCAGGCAGTATTTCTGGCCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT  
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTAGGACCAAGTGGAGTA  
TGATCCCTAACTCCTGATTGATGATCTGAGGGACAAGGGGGGCGGTCTCCGAAGTGGAAATAAATAGGCCGG  
GCGTGGTGAAGTGCACCTATAATCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCAGGAGTTCA  
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAGTGAATAAATGATAATAT

**FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW  
MASRFSRVVLVLIDALRFDAQPOHSHVPREPPVSLPFLGKLSSLQRIEIQPHHARLYRSQ  
VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVMGDDTWKDLF  
PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHHPM  
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAALFLYSPTAVFPST  
PPEEPEVI PQVSLVPTLALLLGLPIPFNGNIGEVMAELFSGGEDSQPHSSALAAQASALHLNAQ  
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
ARAMCIESWARFSLVRMAGGTALLAASCFICLLASQWAI SPGFPCPLLLTPVAWGLVGAIA  
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLLA  
VFFSDSFVVAEARATPFLGSLFILLVVLVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY  
ALRLGIGLLLCRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA  
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAWALASGADEAPPRLRVLVSGASMVL  
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL  
LLHLLAAGIPVTTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPPIHWHAAFVGFPEGHGS  
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEEP  
LMEMLRLDAPQHFFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFIFEAVG  
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271



**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT  
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
ACACGTGGAGTCTTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG  
CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAA  
GATTCTTTGTGCCTGCTGAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT  
TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA  
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAAACACGGAAGGTACTTCT  
CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAAACAGTCATTGAATATGA  
ATATGATGTGAGAACCCTGACATTTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGG  
AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCC  
CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCA  
CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC  
AAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
TATATGTGCAGATGGAAAACTGATGGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAC  
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT  
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG  
GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG  
TGGGTGT

**FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED  
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEWEYDVRTTDCAGPEEQELSL  
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD  
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW  
GLYVQMEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

63/270

**FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845  
><subunit 1 of 1, 283 aa, 1 stop  
><MW: 30350, pI: 9.66, NX(S/T): 2  
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF  
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDIC  
LLRLNGSAVLGPAVGLLRLLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

**Signal peptide:**  
amino acids 1-30

**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
CGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCCGGCGCTGGGCACGGTAG  
CAGGCGCCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC  
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
CGGCAGCAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT  
TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC  
AAGCTGAAAGCCTCAGCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT  
GCCAGAGCAAGCTCGCCATCGTCCTCTTCACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT  
TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA  
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
GGGAGCAGCCCCTCCCCAGATAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
ACCAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG  
GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC  
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
TGTGCACTTGACAGGCCACGTGAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC  
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG  
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
GGTGTCTGCTGAGGGCTTCCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC  
GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA  
TTGCCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC  
TTGCTCATTT

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN  
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD  
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHG STF  
SSTTLGPIFWLLVKSP ELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW  
AESARLVGLEAPSVREQPLPR

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTTCGCGAGCGCTGGCATGTGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
CAGCGTGGCGCGCGCCCTGGCGCCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT  
GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCAATTTACTCTCATCAAACGCCTGCA  
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT  
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA  
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
ATTCATGGCTGGAGGAGGCTGTCACTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA  
ATGTTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
TGAGGCTGTCATCCAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
TATGTGACACCCTGGGTTCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCTCTAT  
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCACCTGGA  
GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
TTGCAGAACCATTGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA  
CCACCGCATTTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
TGGTGAACCTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTACCAAGC  
AGCCCCCTCTACAGAAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
GGTGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
ATGCAGCACTGTTTTGGTGGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
GCTGGCTGTCTGTCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG  
ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACTGAAACTGTTGGCAGAGAGAAGC  
TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCTCGAAATCAGAGGC  
AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG  
AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTC  
TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
GGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG  
CAGGGAGTGTCCCCCTCCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT  
TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
ATGTTTATAAATCAAAA

**FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19



**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG  
CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT  
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC  
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT  
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT  
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCGGAACCAGACCATTG  
ACTTCTGAACGACAACATTGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCCTGGCCTGTGGGGTGCCCTACA  
CCTGCTGCATCAGGAACACGACAGAAAGTTGTCAACACCATGTGTGGCTACAAACTATCGAC  
AAGGAGCGTTTTAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
CTGGTTCATGGACAACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG  
ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA  
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT  
GCCCCACCTGGGGCCTGGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA  
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCCCTCGGGGCAGGAGGGAAGG  
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC  
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA  
GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTAA  
TCAAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAA

**FIGURE 70**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGV PYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN
```

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
CACCTGGGAAGATGGCCGGCCCGTGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC  
TTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGA  
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGACTGTGCCACCAGCCA  
TGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC  
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTCT  
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTCT  
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
TCTGCAGCTTCCTTGACAATGCCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA  
GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTGTGG  
ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA  
GTGAAGCCCTCCGCCCTTTGTTCAACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG  
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAG  
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
CAATAAACACTTGCCTGTGAAAAA

**FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGVTKWFNNSAASLTMTPLDNIPFSLIVSQDVVKAABAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGLIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLT KDALVLT PASLWKPSSPVSQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

**FIGURE 73**

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCCAAAGAAAGAAGGAGATGGTGTATCTGA  
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
CTCCAACCTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGCCATGGTGGATTTTG  
ATGAAGGCTCTGATGTATTTAGATGCTAAACATGAATTCAGCTCCAACTTTCATCAACTTT  
CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT  
CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG  
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC  
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA  
GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCCTTTTATG  
TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
GACTTGTGTGATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
CCATACAGCTTTCTGATGAGTTAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTGTATTAC  
CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA  
ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTGTAAAA  
CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT  
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC  
TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
ACTTTACGCATCTTTCCTTTTGAGTAGAGAAAATTATGTGTGTGTCATGTGGTCTTCTGAAAATG  
GAACACCATTCTTCAGAGCACACGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA  
GATTTTCAGATTCATTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAATA  
TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
TTGTCACTTATTCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
GAGGTGAGGAGTTCGAGACCATCCTGGCCAAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC  
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

**FIGURE 74**

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQLMWETNKRVPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

**FIGURE 75**

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGA  
GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCCTACCGGCGATGCTA  
CTGCTGTGGGTGTGCGGTGGTTCGAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA  
GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGGTTCGTGAGCGACTCCTTCGATG  
GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAACTTCCTTTTATCAACTTTATGAAG  
ACACGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC  
AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAGGGTCTAG  
ATCCAAATTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT  
GGGAAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG  
AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA  
CTAAAGTCAGAGTGATGGAAGGGATTGGCAGAATACAGACAAAGCAGTAACTGGTTAAGA  
AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAAATTTACCACACCC  
TTACCCCTTCACCATCTTCTGGAGAAAATTTTGGATCTTCAACATTTTACACATCTCTTTATT  
GGCTTGAAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTCAGAAATG  
CACCTGTAGATTATTACTCTTCTTATACAAAAAAGTGCCTGGAAGATTTACAÀAAAAAGA  
AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG  
AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAAGTATTGTCATATACTCCTCA  
GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTATAAAATGAGCATGTACGAGGCTAG  
TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGGCCTACAAGTATCAAATG  
TGGTTTCTCTTGTGGATATTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG  
AACCTGAGTGGATACTCTTTGTTGCCGTATCATCAGAAACATTTAAGAATGAACATAAAGT  
CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA  
CCTACATGCTTCGAACTAACCCTGGAAATATATAGCCTATTTCGGATGGTGCATCAATATTG  
CCTCAACTCTTTGATCTTTCCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAATTTCC  
AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG  
CTTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT  
TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAGGAACCAAGGAAGTA  
TGAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTTTGAACAAAAA  
GTTTAAAAATAGTGTCTAGAGATACATATAAATATATTACAAGATCATAATTATGATTTT  
AAATGAAACAGTTTTAATAATTACCAAGTTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC  
CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC  
CAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA  
CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG  
TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTGCG  
AAAAAATAAAAAATAAATAAATAAATTACCAATTTTTTCATTATTTTGTAAAGATGTAGTG  
TATTTTAAGATAAAATGCCAATGATTATAAATCACATATTTTCAAAAATGGTTATTATTTA  
GGCCTTTGTACAATTTCTAACAATTTAGTGGAAAGTATCAAAGGATTGAAGCAAATACTGTA  
ACAGTTATGTTCTTTAAATAATAGAGAATATAAATATTGTAATAATATGTATCATAAAT  
AGTTGTATGTGAGCATTTGATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFINF  
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS  
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL  
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS  
ILPQLFDLSSDPDEL TNVAVKFP EITYSLDQKLHSI INYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97



**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG  
GCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGGTGCCAGCATTGTGACAG  
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCAGGCCATGAT  
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
ATCCTTGGAGGCCTCCTGGGATTCAATCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
ATGTGTGGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG  
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAAACAGCATG  
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG  
ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

**FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886  
><subunit 1 of 1, 230 aa, 1 stop  
><MW: 24549, pI: 8.56, NX(S/T): 1  
MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS  
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAAGATCTTCGCTCCTGC  
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGAGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG  
TGAAGCTGAAGGTTTCAAGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCCCTTGAAGACATAGAAAGAAAATCAACTTTCCTAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

**FIGURE 80**

MVPRIFAPAYVSVCLLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:  
amino acids 1-25

**FIGURE 81**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCTGGAGAAAGAGGCTGGTGTTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACCTTCATT  
CTGTGACCTGTCTGAGGCCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCCTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAACCCTTCACCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

## FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP

LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCCGAGCGCTCACTCGCTCGCACTCAG  
TCGCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCCGGCACCAGAAGTTCCTCT  
GCGCGTCCGACGGCGACATGGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG  
CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGGCAGAACGTCAACCTCACCTGCAGGCTCT  
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT  
CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAAGTGTGTGGTGT  
ACCCATCCTCCTCCCAGGATAGTGAACACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
CTCCAACCGCCGTGCCCAGGAGCTGGTGCAGGATGGACAGCAACATTCAAGGGATTGAAAACC  
CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG  
TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTTCGGAGCCAGCAC  
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT  
CTCCAAACTTTGAGGTCTATAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCCCTCAACCCCTC  
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG  
ATTCTCCCCTAGAGACCTGAAATTACACAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG  
GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC  
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCCACTGGCCATCGCC  
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
ATGTTGCCCCACCACTGGAGATGGTGTCTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC  
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

**FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK  
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRRAQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216



**FIGURE 85**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCC  
TTTCTGCCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
GGTCTGTGGGTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGA  
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTC  
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC  
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACT  
TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG  
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC  
AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCC  
CGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCCTGCCAGACTCCTGCTGCCAAGCCT  
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC  
CCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
GCAGCACAACGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG  
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAA  
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCT  
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG  
CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG  
AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC  
GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCCTGGAGCTGAAGGTCACGGCCAGTCCAGA  
CAAAGTGACCAAGACATAACAAAGACCTAAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHYPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFP SRLPNQCVLC SCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSPDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

**FIGURE 87**

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC  
GTGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCTTGCGGAAAATGCTGATCTCAGT  
CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG  
AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG  
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA  
CGTGGCCTGGAGGAAGAAGTGGATGGTTGGCGGCGAAGGCGGCGCCAGCGGGAGGTACCGT  
GAGACCGGACTTGCCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC  
TTTCTCCTTCGTGGGCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG  
TCCTGTGAGCTGCCGTCGGGTGAGCACGTTTCCCCCAAACCCTGGACTGACTGCTTTAAGGT  
CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAACCAATAAAA  
TCATGTTCTCCAA  
AAAAAAAAAA

## FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

Signal peptide:  
amino acids 1-18

**FIGURE 89**

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCTCGGGCTTGAGGGGAAGA  
GGCTGACTGTACGTTCCCTTCTACTCTGGCACCCTCTCCAGGCTGCCATGGGGCCCAGCACC  
CCTCTCCTCATCTTGTTCCCTTTGTTCATGGTCTGGGACCCCTCCAAGGACAGCAGCACCACCT  
TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCCAGTGCCAGGACC  
AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG  
GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCCTCTCCGGGAGAGTGGA  
TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCAGCTCTGCCCTGTGTAGAGT  
TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAAGGAATGAGAAGTAC  
GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG  
ATTTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG  
TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTT  
GCCATGGCTGCCCCGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCA  
GCTGGTATATGGTGGCTTTCTTTATTTTGCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTG  
GTGAGATGGAGAACACTTTGCAGCTAATCAAATTCACCTGGCAAACCGAACAGTGGTGGAC  
AGCTCAGTATTCCCAGCAGAGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT  
CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC  
ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA  
TGTCCTCAGAGAGAATGCTGAGGCTGCCTTTGTTCATCTGTGGGACCCTCTATGTCGTCTATAA  
CACCCGTCCTGCCAGTCGGGCCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCC  
CTGAACGGGCAGCACTCCCTTATTTTCCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTAT  
AACCCCCGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA  
GATGAGGAAGAAAGAGGAGGAGGTTTGAGGAGCTAGCCTTGTTTTTGCATCTTTCTCACTC  
CCATACATTTATATTATATCCCCACTAAATTTCTTGTTCCCTCATTCTTCAAATGTGGGCCAG  
TTGTGGCTCAAATCCTCTATATTTTAGCCAATGGCAATCAAATTCTTTCAGCTCCTTTGTT  
TCATACGGAACTCCAGATCCTGAGTAATCCTTTTAGAGCCCAGAGTCAAACCCCTCAATG  
TTCCCTCCTGCTCTCCTGCCCCATGTCAACAAATTTAGGCTAAGGATGCCCCAGACCCAGG  
GCTCTAACCTTGTATGCGGGCAGGCCAGGGAGCAGGCAGCAGTGTCTTCCCCTCAGAGTG  
ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTCTGTCTCTCTTCTCACTCCTCCCT  
TCAGTGTCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTGCAATAAA  
AGGAAAATCCACAAA  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM  
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVRVFPFWVGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTAQ  
QWDTPCPRENAEAAAFVICGTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAG  
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT  
CCGTACCTCTCCTGTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG  
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTTCTCCTGTTTCCTGTC  
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
ACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC  
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA  
TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCATACAGGGATATGTT  
GATAGAGACATCCAGCTACTCTGTCACTCCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG  
GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA  
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATCCAGGCGGAAGTGGAC  
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC  
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTGAACCCATA  
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
TCTCAGAGTTTCCAAGCAGGGAAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCCG  
ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGACTATGAGTG  
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCCGT  
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAATCCC  
ATAGTCATCTGCCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC  
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
GTGAAATGTAGGATGAATCACATCCACATTTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC  
ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACC  
TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACATTTTCAGTA  
AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRIS SQSYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFP RP TAKWKGPQGQDLSTDSRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAE LDWRRKHGQAELRDARKHAVEVT LDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFRTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVC RDDVD RRKEYVTLS  
PDHGYWVLRLNGEHL YFTLNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATTPFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255



**FIGURE 93**

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCCGATTGCA  
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG  
CCGTGCGCTCAGCCGCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG  
GACGCGTGC CGGGCCCCGGGTTGCGGGGCGAGCCCAGCCACCCCTTCCCTAGGGCGACGGC  
TCCCACGGCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
CGACTTCTCCAGCCCAGTCCCCGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCC  
ACCACCTTTCAGGCGCCGCTCGGCCCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC  
GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCCG  
CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCC  
GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC  
TTCGCTCCTCCAGAGTATGTATGTAAGTCTGTGTTGGAAGCCTGAATGTGAATCGCT  
GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC  
ACATGGAGCTCTCAGCATAACCGTGCAACAGGTAAGCAACAGAGGGTGGAAGTGAAGTTTATT  
TTATTTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
GAGGATGAGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT  
TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTTCCTTCAAAAGCACTAG  
AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAAT  
AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA  
ATCAAAATTTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA  
TTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGACCAAAAG  
TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA  
ATAATGTACTGTTATCTAAGCATTTGCCTTGTAAGTCACTGAAAGTAATTTCTTTGACCT  
TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAAT  
AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC  
CACTTACGAGCTGTGTTCTTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTCCTTCTCAAG  
GTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
TTCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA  
ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA  
TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG  
AGGCTGGGCGCGGTGGCTCACGCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT  
CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA  
AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT  
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT  
GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAA

**FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRS LPSLGGLALLCCAAAAA VASAASAGNV TGGGGAAGQVDASPGPGLRGEPSHPFPRATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTDLPSSSNSSVLPTPPATEAPS  
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCAGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTCACAGTAGCAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTC  
CACAGCA

## FIGURE 96

MGGLLLAAFLALVSVPRQA VWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVG VVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAI IFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCC  
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
GGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
GATTCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA  
AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
GCACCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
GGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTG  
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC  
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
AGAGCAAAGCCACATCAGGAGTGAATCAGGGGGTGGTCCGGGGGAGCTGGAGCCACAGCCCTG  
GTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGAGGAAGAAATCGGCAAG  
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGTTTCAGCCT  
CTCAGGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT  
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
ACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGA  
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

**FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
SIKWNKYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVSPWACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTLLIPQPQDHGTS LTCQVTFPGASVTTNKT VHLNVSYPPQNLTM TVFQGDG  
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGDTGIEDANAVRG SASQGPLEPWAEDSPPDQPPPASARSSVGE GELQYA  
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCTGGAGATGAAGACCCTGTTCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCTTCACCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGG  
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

**FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:**

**Signal peptide:**

amino acids 1-17



**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTTGAGCACCA  
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGA CTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT  
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA  
CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT  
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV SITW  
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLR CANITIEHQK CENAYPGNITDTM  
VCASVQEGGKDSCQGD SGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTGTCATCGTCCAGAAAAC TGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCTTGGTGTTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATAACCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTGT  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTAAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT  
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCCTATGAGAAGATATTTTGA  
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLVGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG  
YLAKDGSKFYCSRTQNEGHPKWFVLGVGVQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDIFKKNDHGDGDFISPKEYNVYQHDEL

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

104/270

**FIGURE 105**

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAACCAAACCTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC  
CCTTGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCAGTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA  
AGTACTTATATTCTC

**FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL  
ETCNARHGGSRL

Signal peptide:  
amino acids 1-18

**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG  
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
CAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCTCCGCGTAACCAGCAGCGTTCAAC  
CCCTGCCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC  
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGAGAATCACGAGCAACATGGTGTGTGCAG  
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC  
CTGTTTCTCCACCTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACC  
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACCTTCTTGGAACCT  
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

## **FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCQDGI PGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17



**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA  
ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCCGGCAGGAGAGGAGGCTGGCC  
GAGATCAACCGGGAGTTTCTGTGTGACAGAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA  
CATGATGCTGGGGAAACGGTTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGA  
GGACCCCGCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTTT  
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGGGGGAATCC  
TGAGCCTTGGGTCCCCCTCCTCTCTTCTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG  
ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTTCAAGAAAGTCTCCAAGCCAAGTTTCAAGGCTC  
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCCC  
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
TACCAGAAGGAACCCCTCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG  
GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 110**

MSGELSNRFQGGKAFGLLKAQERRLAIEINREFLCDQKYSDEENLPEKLTAFKEKYMEDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRS AVLKLV  
MFEGKANESSPKPVGPPPERDIASLP

**FIGURE 111A**

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCGAGAGGCAGCCTCCTCCA  
GGAGCGGGGCCCTGCACACCAATGGCCCCCGGGTGGGCAGGGGTGCGCGCCGCCGTGCGCGCC  
CGCCTGGCGCTGGCCTTGCGCTGGCGAGCGTCTTGAGTGGGCCTCCAGCCGTGCGCTGCCC  
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTC  
CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC  
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACCAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA  
AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT  
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCAACCAGC  
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT  
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
TGCCAGCCCCCCTCGGAGCCCCATCCTGCAATGCCAATCCATCTCCTGCCCTTCGCC  
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCCTGCCA  
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA  
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA  
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT  
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCCGCGCCG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG  
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC  
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT  
GGAGACCGTGACGGGCGCGTGTTCCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACGCTTGTCTCCCT  
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCTC  
AAGGAGATTTCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGACCTGTATGGAGACAGTGGTGGCAT  
GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC  
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC  
GGGCTGCGGTCCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTCCCTGAAGG  
CTCCTTCAACGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCTGCTCCTGCCCTC  
TGGGCTTTGAGGGGACGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
AACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCTAACTACAC  
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTTCAGCATG  
AGGCCAAGTGCATCCCCCTGGACAAAGGATTCTGAGTGTGCGAGTGTGTCCCTGGCTACAGCGGG  
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGGCCAGTG  
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCTTCTGTG  
AACACCCCCCACCCTGCTTACTGACAGACAGCCCATGCGACCAGTACGAGTGCCAGAAC  
GGGGCCAGTGATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCCG  
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG  
CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC  
GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACAGGGCCACGT  
GCGGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA  
ATGATGGGCAGTTTACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG  
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGCCTCTCCGCCTTGCGCCAGGGCACGG  
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGT  
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
GCTGGACCGGCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
CATGGAAAATGTGTGGCAACTGGGACCTCATACTGTGCAAGTGTGCCGAGGGCTATGGAGG  
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCATG  
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC  
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT  
GTGGGCCCCAGTGCTGCCAGCCACCCGAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG  
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC  
CTAAGGCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAA  
AAAAAA

**FIGURE 112**

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL  
PELLFQSTPKLTRLDLSENQIQGIPRKA FRGITDVKNLQLDNNHISCIEDGA FRALRDLEIL  
TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL  
RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
EIRLEQNSIKAIPAGAFQYKKLKRIDISKNOISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL  
AQNPFFVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
SNDTFAGLSSVRLLSLYDNRIITTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR  
IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGLR  
ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL  
SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCSLRWL  
SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHR FQCKGPVDINIVAKCNACLSSPCKNNGT  
CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR  
CEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLCQHEAKCIPL  
DKGFSCECVPGYSGLKETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV  
LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS  
VELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD  
QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ  
PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG  
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGA AAAAAGGCTGTGAGGTTTCCTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA  
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCAT  
TTAAATGTC

## FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:  
amino acids 1-19

**FIGURE 115**

CAGGCCATTTGCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCTATTAAACTTGTACATGGCTCCC  
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC  
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG  
CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
TTATGACGAGAGAGTCTTGGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC  
CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTCTGGGTGGACCCTTGGAGT  
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA  
ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG  
AGTGAAGGAAAAATTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC  
TGCTGGTATAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
CAGTTTTGAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA  
CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCAA  
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT  
CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTGTGTTGTCTTGTCTTGCCTGGATC  
CATAGCGAGAGTGCTCTGTATTTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA  
TAAAAGGTGTTTATCATAAAAA



**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLARRRKKILFYCHFPDLLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTTGGACTTCGCGATCTT  
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT  
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
ATATCAATCCCAATAAGACATCGGACCCTTTTGAACCATGCTGAAGTCATTATTAAGGTAT  
CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT  
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCT  
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGGTCTAC  
TTGATAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC  
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA  
GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTTACTCC  
AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTTCGAACTGCCA  
AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT  
CCTAGAGAGACCCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCTCT  
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTATTGA  
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
ATTAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACATTTAAAAA  
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
TTAA

**FIGURE 118**

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVSVSLGTVDVLKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTTSSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL  
QDPNTWPSPHKFPDRFDDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTTCAGCTGG  
TGGCCGCGCTCTCTGTCAACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCT  
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA  
AAGAAACCCTTCTTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCTTGGAAGAAGGAAGGCATAGGCTTCGGTTTTTCCCTCGGAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTTAGGGGACA  
ATTAAAAAAAAAAAA

## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACTATGTCCCGCCGCTCTATGCTGCTTGCCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAAC TTCACGGGTGC  
CCACTCAGGTCAC TTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC  
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

## FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

Signal peptide:  
amino acids 1-20

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT  
GACTCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
ATGATGGTCTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCQGGACCTC  
GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCCTACTACCCATC  
TGGGTTGACCCGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG  
ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
CTGGTCCCAACCTGAAGCTGTGGAGTGAAGTACATCAGAGGAGCACTGGAGGAGGAGTGGGCT  
CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG  
TCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGTGCTGAGCATG  
GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCC  
ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC  
CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA  
GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT  
GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT  
GCCCCGGGGCA



**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR  
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY  
YPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA  
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTGACCTAGCCGCTAG  
CATCTTCCCGAGCACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
GGCTGCGGCTGCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
GCCGTGCTGCTGGTCCTCACGCTGCCGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCCTTCTCG  
GCGGTGCGGAGCACCACCGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
CGATCAGATCCTGGTGAATGTGGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA  
GAAAAGGAATTTACAGTTTTCAGTTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG  
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
AGTTATTGGAAGATCATTTTTTTCATCATTTGGATTGATGTCTTTTATTGGTTTTCTCATGGGTG  
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTTCACAGATTATTTGTG  
TGTGTCTGTTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT  
TACAGATGTGGAATTTTATTTGTTTTAGTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA  
AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTTTTGGTTCTTGTA  
AAAACCTGGATTTTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA  
TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA  
GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT  
TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC  
TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTTT  
TCCGTAGACATGACCCTTTATTAAGTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA  
TTAATATATGTTAAAAAA

## FIGURE 126

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSSPLGI  
SVRAANSKVAFAVRSTNHEPSEMSNKTRIIFYDQILVNVGNFFTLESVVFVAPRKGIIYSFSF  
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

**FIGURE 127**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCT  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

**FIGURE 128**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLG  
GIMSGVFSFVNTLSDSLGPSTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKK  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKCLLCQDKN  
FLLYNQRSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65



**FIGURE 130**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659  
><subunit 1 of 1, 832 aa, 1 stop  
><MW: 94454, pI: 6.94, NX(S/T): 12  
MFALGLPFLVLLVASVESH LGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT  
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE  
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQRPQYFKYEFPEGVDSVI  
VKVTSNKAFFPCSVISIQDVLCPVYDLDDNNVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV  
VKTEDQACGGSLPFYFPAEDEPVDQGHRQKTL SVLV SQAVTSEAYVSGMLFCLGIFLSFYLL  
TVLLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL  
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL  
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYNFLCAHPLGN  
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGFLFYAMGTALM  
MEGLLSACYHVCPTYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS  
VLGVVFGKGNTAFWIVFSIIHIIATLLLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG  
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI  
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDDFFDDHDIWHFLSSIA  
MFGSFLVLLTLDDDLDTVQRDKIYVF

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGCCTTGCCCTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG  
ACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC  
CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC  
TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCA  
GGCAAGGCAACTGAGGGGCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG  
GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCAACCCTGGAGATGCAGGATG  
GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
CTTCCTCTTCTTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT  
TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
GAGAATCTCAAAGTCTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT  
GCACTATCACCTGGAGAGCCATCCCCCGGACCCCTTGAAGTGAATGCAGAGGGAAACCTCT  
ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
AATTCCTATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
CAGGTAAGTGAAGTGAAGTACTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAAC  
CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAAC  
TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCTGAGTTCATCACTTCCCAGAT  
TGGGCCATATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA  
TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC  
AGCCGGCTCTTCTGCTGACCATCCAGCCCTCCGACCCATCAGCCGAACCCTCAGGTTCT  
CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATCTCCGGGGAGGTGCACACC  
GCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA  
TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG  
GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
TTCACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTT  
CCATGCCTACCTCACCTTGGCCCTGCATTTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTTCGAGTGATCGTGTGCTGCAAC  
GTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTGCGC  
AGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCTCATCCTCATTTTACCC  
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCCTGAAGGCG  
ACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
CTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCAT  
CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAAC  
TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCA  
GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG



**FIGURE 132**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGRTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFMFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSIIESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLMVDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH  
VYQQLLSPEPEDGVEGRAFGVDPTSGSVTLGVLPFRAGQNIILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADLEPAFRLMDFAIERGDT  
GTFGLDWEPPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISTRFLRSLVNDSEGWLCKEKFSGEVHTA  
QSLQGAQPGDITYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIIPVVVSHNAQMWQLLVRVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTGAGTCTGCAGGCATTTAAATCCTTCCTG  
AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA  
AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG  
CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTGAC  
CTGGCGAGGAGGGTGAAGATTGGACATTCTGTTTGA AAAACCGGCCGATGTATGTACTGAAGTT  
CAGCACTGGGAAAGGCGTGAGGCGGCCGCGCTTTGGCTGAATGCAGGCATCCATTCCCAG  
AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTGCCTGTGGCCAAATCC  
TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCAGAAATC  
CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGTCAGGAAAG  
GGAGCCAGCGACAACCCCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA  
GGTGAATCAGTGGTAGATTTTCATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGCACTGA  
GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC  
TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGCATGGCTCTGCTCTGTCTACATTTAT  
TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG  
TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
CGTGTGTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCTG  
CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACCTC  
AGCATACCCCTTCCCTGGGTGGCATGTCTCTCTCTACCTCATTTTTTAGAACCAAGAACATC  
TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
GTGGGAGACACCACCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT  
TCGCAGTCTTCTGGAAAATATTTTCTTTTGTAGCAGCAAATCTTGTAGGGATATCAGTGAAG  
GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTTTGTAGACAGAGTTTTGCTCTTGTGTC  
CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCA  
ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA  
ACCTCAGGTGATCTGCCCTCCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
TGCCGGGCCCCGTCCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCAC  
TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAAGTGTG  
ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
GTGACCATCTAAATTGCAGGATGGTGAAATTATCCCATCTGTCTTAATGGGCTTACCTCCT  
CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAATCACTCAT  
CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGTGCTGTGGTGTATCCTGTGTT  
TCCTTGTCCTGGTTTTG  
TCTGTCTATTTTGTATCCTGGACCACAAGTTCTTAAGTAGAGCAAGAATTCATCAACCAGCT  
GCCTCTTGTGTTTCATTTACCTCAGCACGTACCATCTGTCTTTTGTGTTGTGTTGTTTGTGTT  
TTGTTTTTTTGTCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA  
GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

**FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNL

**Signal peptide:**

amino acids 1-16

**FIGURE 135**

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTC~~CAAAATG~~  
GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC  
CCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCAC  
AGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGTTTTGAGAGACC  
CCGAGTCAGAACATCTTCTTCTCCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT  
TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA  
CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCAGC  
AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC  
AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA  
ACCCCTCCATTGCCCGAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCCAAGGGAAGGTT  
GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT  
TAAAGCCAAGTGGGAGAAGCCCTTTACCTTGAATATACAAGAAAGAACTTCCCATTCCTGG  
TGGGCGAGCAGGTCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGG  
GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT  
CTTTGTCTCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACAC  
TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTATCCCCAGATTTTCC  
ATTTCTGCCTCCTACAATCTGGAAACCATCCTCCCGAAGATGGGCATCCAAATGCCTTTGA  
CAAAATGCTGATTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC  
ACAAGGCTGTGCTGGATGTGAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG  
TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCT  
GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCA  
CTAAATCCTAGGTGGGAAATGGCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAA  
CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCAGTGGAGCTGGATTCGCTG  
GCAGGGATGCCACTTCCAAGGCTCAATCACCAAACCATCAACAGGGACCCAGTCACAAGCC  
AACACCCATTAACCCAGTCAGTGCCCTTTTCCACAAATTCTCCAGGTAAGTACTAGCTTCATG  
GGATGTTGCTGGGTTACCATATTTCCATTCTTGGGGCTCCAGGAATGGAAATACGCCAAC  
CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAACTAAAAATATGAAT  
TCAAA  
AAAAAA

**FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

**FIGURE 137**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGC  
CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG  
CCTTTATCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAG  
TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGC  
AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC  
AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC  
CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA  
GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGG  
ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA  
CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC  
CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC  
ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA  
GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA  
GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC  
ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
CACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGG  
CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAAC  
TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC  
CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCA  
CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAG  
TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCTCCAG  
TGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCA  
CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC  
ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC  
TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT  
CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACT  
TCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC  
AGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGAAGCAA  
AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCCTCATCACCTGGTCTCGGTGTGGCG  
GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC  
CTTTAACACAGCTGTCTACCACCCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG  
GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCCTAACTGGTTCTGGAGGAGACCAGTA  
TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTGAGCAGCCCCGGAAGCAAG  
TGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTTTCATTCATC  
CCAGGAGACCCCTCCCAGCTTTGTTTGGATCCTGAAAATCTTGAAGAAGGTATTCTCACC  
TTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA  
ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAG  
CTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA  
TCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI  
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST  
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAGLFFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFWRPVSIIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCTTAAACTGGCATCCGGCCTTGTCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC  
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTTGTGAATAAACTTGATACACCA



**FIGURE 140**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
REVEKVFENGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGVNQASKEANQLLNNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

141/270

**FIGURE 141**

CTCCGGGTCCTCCAGGGGCTGCGCCGGGGCGGCTGGCAAGAGGGGACAGTCTAGTGGGACCTCCAGGAAGAGCGGC  
CCCGCGGGGGGCGATGACCGTGCCTGCTGACCTGACTACTCCAGGTCCGGAGGCGGGGGCCCCCGGGGCGACTCG  
GGGGCGGACCGCGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTCTC  
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCTGAGGAGCTGGCTCGCCGCCCCATGGGGCGCTGCCG  
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGTCAGCCGCCGCTCCGACCTGGGCGCTCAGC  
CCCCGATCAGCCTGCCCTCTGGGCTCTGAAGAGCGGCCATTCTCTCAGATTCTGAAGCTGAACACATCTCCAACCTAC  
ACAGCCCTTCTGCTGAGCAGGATGGCAGGACCGTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC  
AACCTCAGCTTCTCTGCGCAGGCGGGGAGTACCAAGAGCTGCTTTGGGGTGCAGCAGCAGGAAGAAACAGCAGTGC  
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTGCAAAACATACATCAAGTCTCTCGCGCTCAGCGGACGTACG  
CTGTTTCACTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCTTGGCAAGG  
GACGAGAAGGGGAATGTCTCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC  
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC  
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC  
ATTCTGAGAGCTGGGACAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA  
TTTGAGTTCTTTTGAGAACCAATTGTGTCTCCGCAATGCTCCGCGATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG  
CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGTGTGCTGTGCTCAGGCCCGACAGTGGCTTCCCCTTCAAC  
GTGCTGCAGGATGTCTTCAGCTGAGCCCCAGCCCCAGGACTGGCGTGCAGACCTTTTCTATGGGCTCTCACT  
TCCCAGTGGCACAGGGGAACCTACAGAAGGCTCTGCCGTCTGTGCTTTCACAATGAAGGATGTGCAAGAGTCTTC  
AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG  
CCTGGAGCGTGTCATCACCAACAGTGCCCGGGAAAGGAAGATCAACTCATCCCTGCAGTCCCAGACCGCGTGCTG  
AACTTCTCAAGGACCACTTCTGTAGTGGACGGGCGAGTCCGAAGCCGATGTGTGCTCTTCTGGGCACTGGTGAC  
TACCAGCGCTGGCTGTACACCGCTGCCCTGGCCTGCACACACATCATGATGTCTCTTCTCATCGGGA  
CAGCCCGTGCAAGTCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCCTACACTCGGGCGTAGTCCAG  
GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGGACTGCCCTCTCGCCCGGAGCCCTACTGTGCTTGG  
AGCGGCTCCAGCTGCAAGCACGTACGCTCTACAGCCTCAGCTGGCCACAGGCCGTGGATCCAGGACATCGAG  
GGAGCCAGCGCCAAGGACCTTTGAGCGCGTCTTCGGTTGTGTCCCGTCTTTTGTACCAACAGGGGAGAAGCCA  
TGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA  
CTCTGGCTACGCAAGGGGGCCCCGTCAATGCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG  
GTGGGCACCCAAACAGCTGGGGGAGTTCCAGTGTGCTGCTACTAGAGGAGGGCTCCAGCAGCTGGTAGCCAGCTAC  
TGCCCGAGAGTGGTGGAGGACGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA  
TCGCGTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGTCTTACTGGAAGGAGTTCTCGGTG  
ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA  
GTCTTCTTGAAGCAGGGGGAATGTGCGACCGTGCACCCCAAGACCTGCCCTGTGTGCTGCCCCCTGAGACCCGC  
CACTCAACGCGCTAGGGCCCCCTTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG  
GGGGCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGACTCAAGACAGTCTCGTGAGGATATCCCCAGTG  
TGCCCCCGGCCCCGGGTCCGCCCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTCCAGGAGC  
TGCCCTTGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGTGAAC  
ACGACCGTGGTGGCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCAGTCAAGTAGCGAAGCTCC  
TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGTCTTGCCCAAATATGGGGGCTGCCTAGGTTGGTGGAA  
CAGTGTCTCTTATGTAACTGAGCCCTTTGTTTTAAAAAACAATTCCAAATGTGAAACTAGAAATGAGAGGGAAGAG  
ATAGCATGGCATGCAGCACACACGGCTGCTCCAGTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG  
TTGTCTGAGACAGAGTTGGAACCTTACCACTGTCCTTCTTCACTTCCACATTATCCCGCTGCCACCGCTGCTG  
CCTGTCTCACTGCAGATTCAAGACCAGCTTTGGGCTGCGTGGCTTGCCTTGCAGTCAAGCAGGAGTGTAGTTG  
TTGTGCGCGTCTGCTCCACCACTCAGGGACCAGAGGGCTAGGTTGGCAGTCCGGCCCTCACCAGGCTCTGGGCT  
GGACCCAACTCCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA  
TTTCGTGACAATGTACGCCCTTTCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCTTCTCCGTTGTTGCGTGA  
GAACCCGTGTGCCCTTCCACCATATCCACCCTCGCTCCATCTTTGAACCTCAACACAGGGAACCTAACTGCACC  
CTGGTCTCTTCCAGTCCCACTGATGCTACCTTCCATCCCTCACCTTCTCCACTCTAAGGGATATCAACACTGCC  
AGCACAGGGGCGCTGAATTTATGTGTTTTTATACATTTTTTAATAAGATGCATTTATGTCAATTTTTTAATAA  
GTCTGAAGAATTACTGTTTTAAAAAATAA

142/270

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962  
><subunit 1 of 1, 837 aa, 1 stop  
><MW: 92750, pI: 7.04, NX(S/T): 6  
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCF  
FDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP  
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLLLVGTTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVIIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVFLFLLYRHRNSM  
KVFLKQGECAVHPKTCPVVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGAGGATGTGCAGCTGCGGCGGCGCGCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACC GA  
GCCCAGCCAGCCGAGGACGCGGGCAGGGCGGGACGGGAGCCCGACTCGTCTGCCGCCGCGCTCGTCCGCGT CG  
TGCCGGCCCCCGCTCCCCGCGCGAGCGGGAGGAGCCGCCACCTCGCGCCGAGCCGCGCTAGCGCGCGC  
CGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGCGGGG  
CCTGCGGGCGGCTCGGGGCGCGATGGGCGCGGCGGGCCCGCGGCGGCGGCGGCTGCCCGGGCGGGGCTCG  
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGCGGCGG  
GGCGGCGGCGGCGGCGGCGGGCGGAGCGGCGCGGGCATGGCGCGCGCGGCGGCGGCGGCTGGCTCAGCGTGC  
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG  
GCCCACGGCGCGCGCCAGCCCCGAGGGCTGCCGCTCCGGGACGGCGGCGGCTTCCAGGCGGCGGGCGCGCG  
GCGATGCGCGCGGGGCGCAGCTCTGGCCGCGCGGCTCGGACCCAGATGGCGGCGGCGGCGGCGGCGGCGG  
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA  
TTCTTGGGAAAGTTCAGTCTTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG  
GTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA  
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAATTCCTGAGGAGTT  
TGAACAGCAGCGAGCCCTCTTCTTGGGCGAGCAGGCGCTGGGCACCACGGAAGAAATGGGAAAATGGCCCTGG  
AGCCTGGTGAGAACTTTCGATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCCGAGAATGGTGCCGC  
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCGGAGGTTTG  
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCGAGCTTTTTTATGAGAATTACGAGCAGAACAAAAGGGGT  
ACATTAGAGATCTCATAACAGTAAAATTACCAAGCTATCACATTACCCCCAACAAAACCCACCTTACCAGT  
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA  
TTGTCTGATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA  
TGAGGTTTCAGCCCCGCGAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTCCGGCAG  
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCCAGAGGGAAGCCTTGAGCGACATTGTCTGCAGGTCA  
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGCGGCATCTTGACTTCAAAGAGATCCAGTACGGCTACCGCC  
GGGTGAACCCCATGTATGGGGCTGAGTACATCTGGACCTGCTGCTTCTGTACAAAAGCACAAAGGGAAGAAAA  
TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC  
TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAATCCCTGAAGA  
AGCTCGTCCCCTTTCAGCTCCCTGGGTGGAAGGTGAGCACAAAGAACCCAAAGATAAAAAGATAAACATACTGA  
TTCCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC  
AGAAGCTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCTGACAAGGCCAAACAAGTTGAACTGATGA  
GAGATTACCGCATTAAGTACCCTAAAGCCGACAGGCGAGATTTTGCTGTGTCTGGAGAGTTTCAAGGCTTGG  
CCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTCTGCGACGTGCGACCTCGTGTTTACTA  
CAGAATTCCTTCAGCGATGTGAGCAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT  
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTGCTTTTACTCAGAAAATGGCTTCT  
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA  
TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC  
AGGAAGTAGGAGTAGTCCAGTCCACCATCCTGCTTTTGTGATCCCAATCTTGACCCCAAACAGTACAAAATGT  
GCTTGGGGTCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTT  
TAATTATCTAATTTATTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC  
AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGCTTTGAA  
CACATCTTCTGTGAACATTATGTAGCAGACCTGCTTAACCTTGACTTGAAATGTACCTGATGAACAAAATCTT  
TTTAAAAAATGTTTTCTTTTGGAGCCCTTTGCTCCAGTCCATGGCAGAAAACGTGAACATTCTTGCAAAGTAT  
TATTGTAACAAACACTGTAACCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTGT  
GTTTTGTTTTTTTTTTTACAATGTTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA  
GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC  
CACGTAGGTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGAGACGGAGTCTCACTCTGTTACCGAGGTGAATG  
CAGTGGCGCAATCTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATCCCTGCGCTTTGCTTCCGAGT  
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTGTATTTTTTAGTAGAGACGGGGTTTACCAT  
GCAAGCCCAGCTGGCCACGTAGGTTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTCTCG  
TGTAGTTTCATTGCGCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTTGGCATTCTCTCTTCTGACCTT  
CTCTTTAAAGGGTAAATATTAATGTTTAAAGTGAACAAGATGAATTATTACAATAAATCTGATGTACACAGACT  
GAAACATACACACATACACCCTAATCAAAACGTTGGGGAAAAATGTATTGGTTTTGTTCTTTTATCCTGTCTG  
TGTTATGTGGGTGGAGATGGTTTTTATTCTTTTATTACTGTTTTGTTTTATCTTTGTATCTGAAATACCTTTAA  
TTTATTTAATATCTGTTGTTTCAAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTATCGG  
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACGATCTCAAAGATTTCTTTTGGAAACGCTTTTTTCCCTCC

144/270

**FIGURE 143B**

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG  
GACAAAAGTGAAATGAATCTGTCAATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTGGAATAAACCAGTGAACAATATTTTCTATTGTACTTTTGAACCATTTGTCTCATT  
ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAATTAAACACGAAAAA

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRRAWLSVLLGLVLGFLVSLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG  
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFWMRADDVYIKGDRLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT  
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE  
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPYGAEYILDLLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFSLNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESSLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDDVDFNKKVVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

146/270

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC  
TAACTCTCCAAAACATGTTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
ACTTTCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC  
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCAGAGAGTTGGAATAAT  
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTTCTTAGTGA  
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA  
GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTC  
TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG  
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
AAAGTTTATTAAACAATAATATAAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA  
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTATGTGTATGAACA  
ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAA

**FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNP ISEETTTFTPTGGFTPEIGKKKHTESTPFWSI  
KPNNVSIVLHAEOPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL  
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19



**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACA  
GGAATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG  
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
GTATCGAGGGAGAAGTGAAGTTTGTGAAGGACTCCATTGCGGGGGCGTGTCTCTCTAAGGC  
TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTAC  
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCTCCAGC  
CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA  
GGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG  
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
ACTGTAAACCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC  
AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG  
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC  
ATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
CTGCTGACATGTGAGTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGA  
GAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTTGGGGATGAGACAGAGAAGACCCTG  
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC  
CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCCTTTAGGGAGC  
TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCAGATGAGGGGGGAT  
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGA  
CAACGAATGTGAATCATGCTTGCAGGTTTGAAGGCACAGTGTGCTAATGATGTGTTTTTA  
TATTATACATTTTCCCACCATAAACTCTGTTTGTCTTATTCCACATTAATTTACTTTTCTCTA  
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG  
GAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAACCAGGCAAAG  
AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAAACACAGACACAAAA  
TTCTAAATAAAATTTTAACAAATTAACCTAAACAATATATTTAAAGATGATATATACTACT  
CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGTGTAATT  
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

**FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALC  
GVVMGMIIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS  
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
GGAAAAGAGTTTGTGGGAACCCCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGTC  
CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA  
TTACTATAGCACATTGTCAATTACAACTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
AGTGTTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG  
ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA  
GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
TTGCTGCGGAACACGAAGAAGTAAAACCTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG  
AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT  
CTTGACAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG  
CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGGTGTGGAGGCCATT  
TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
TGTTTGCTTGATGCATGTATTTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
CCAGATCAACTCTGTCTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGAGAATTTTGAC  
TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAGGAGTGAAAGAAAATA  
TAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
GGAATATTAGAAATGATCATATTCAATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
ACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
TCCTTATTTTCAATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTG  
ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTTCTAAGCAAATTAAGCAAATAT  
TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

**FIGURE 150**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD  
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR  
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL  
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG  
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDV  
MFVTGFGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD  
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

**FIGURE 151**

GTCTGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCCC  
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCCACTACTGG  
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTTATGTGCTTTGCGTAGTGGCCGCTA  
ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
CCTGCCTTCGGGCCTTGACGCCGCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC  
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCCTGCGCGATCGCTGGGGCTGCCCCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTCTTGA  
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTAA  
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAFPSPVLHYWLLLLWDGSEA  
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRV PQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTL VHAAVGVGTALALLS CAALVWHFCLRDWGCPRRAAARAAGAL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
CTGCCCCGATGAGCCCCCGCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGCGGCACCGGG  
CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC  
TTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGA  
TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
ATTTTGACTTACTTTCTGTGGTTTCATCCGGTCATGATTGCTGTTTGCTGTTTCTTTATCAT  
TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT  
TTGGAAGTTTGCTTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG  
GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACCTTGAAGCCAGGATGACAAATTA  
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGAATTTTTTTCAGAGAGAGTTTAAAGT  
GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT  
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGA  
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACTGC  
AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTTCTCACC  
ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAAATGATGTC  
CTTGAAGAATGACAACTCTCAGCACCTGTCTGTCCTCAGTAGAACTGTTGAAACCAAGCC  
TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTTGAGATGGAG  
GAGTTATATAAAGAAATGTACAGAAGAAAACCAAACTTGTTTTATTGGACTTGTGAATT  
TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA  
CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC  
CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT  
CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT  
CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAACTTTC  
AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA  
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
TCTGTATAATTGAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
ATTTGTCTGTATAGCATCATTATTTTTCAGCTTTCTGTTAATAAAGCTTTACTATTCTGT  
CCTGGGCTTATATTACACATATACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA  
CCAGTGTGATACATAGGAATCATTATTGAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA  
GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG  
AAGACTCTTTTTGACACTAAACACTTTTTTAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA  
GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAT  
GCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTCTACTGATTA  
ATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAAGAGTATAGTATATTTATTT  
GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTGTTTATTTCTCAGAATATGGAA  
AGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA

**FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV  
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ  
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF  
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL  
YYDRREPGETDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG  
TGATTCTGGATAAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG  
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
CCCCGAAGGGCCTGCAGTGCGAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
ACTCGGCCACAGGGAACTGGTTCTCTGCCTGTTTTGACAACTTCACAGAAGCTCTCGCTGAG  
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA  
TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGGCCCTGTC  
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGT  
GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGA  
CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCAGGCGAGCCCACT  
GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC  
AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAA  
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGC  
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA  
TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC  
CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
GGGCCCCGAGCACCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTG  
CCCTGCCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC  
CTCTGCCCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC  
TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC  
AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
GGAACTTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG  
CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA  
CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
ACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
CTGGCAAAAAAAAAA

**FIGURE 156**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTQCQGDSSGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

**Transmembrane domain:**

amino acids 32-53 (typeII)

**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG  
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC  
TTTTCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCATGCCCA  
GGGTGAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCTCCAGGATTTTGACA  
CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG  
ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA  
AGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCTGGTTTTCTTACAATGTCACCCATCTCTACA  
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTTACCTGTTGCCCATCTCGG  
AGGACAAGGTTCATGGAGGGAAAAGGCCAAAGCCCCCTTGACCCCGCTCACAAGCATACGGCTGTCTGGTGGATG  
GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGC  
CTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCTCCTTTGTGGCAGCCATCCCTTCGACCC  
AGGTCGTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGG  
CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGTGTCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGC  
TGCTCTGACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCGGATTCTCCCA  
CAGCTCCCCACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCCT  
TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  
CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCTCTGATAAGGCCCTGACCT  
TCATGAAGGACCATTTCTGATGGATGAGCAAGTGGTGGGGACGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATA  
CACGGCTTGCACTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCAACACAG  
GGTCGCTCTCAAGGCTGTGGTAAGTGGGGACAGCAGTGTCTCATCTGGTGGAGAGATTGAGCTGTTCCCTGACC  
CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCAGGCTGTCAGTGTGTTGTAGGCTTCTCAGGAGGTGTCTGGA  
GGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCACTGTGCCT  
GGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCCTGGAAGCAGGACATGGAGCGGG  
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAATCATT  
AAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGTCCCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT  
GGAGTCATGGCCAGCAGCAGTCCAGAAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGG  
ATGGAGTTGGGGTCTCTACCAAGTGTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG  
ACAGCCAGGACCAGACCCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA  
CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCTTACTGGCCCCACTTTGTCACTGTCACTGTCTCTCT  
TTGCCCTTAGTGCTTTTCAAGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG  
TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG  
AATGCAGGACCTCTGCCAGTGTGTGGACGCTGACAACAACCTGCCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  
CAGGCCCGGGCTGCGGTGACAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG  
CAGCACAAGAGACACCTTTCTCCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  
ATGCACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC  
CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCTC  
CAGAAACACAGTGTTCAGAGACCTTAAAAAACCTGCTGTCAGGACCCCTATGGTAATGAACACCAACATC  
TAAACAATCATATGCTAACATGCCACTCCTGGAACTCCACTCTGAAGCTGCGGCTTTGGACACCAACACTCCCT  
TCTCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC  
TTTCTGAAGTCTGACCACCTTTCTTCTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG  
CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGT  
TTTGGGATTGAGAAAACCTGTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTAAAAAAA

**FIGURE 158**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEKGKQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFLVLSGALIIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

**FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
TGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTC  
TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG  
TGGCAGAGGAAAATTTGAAAACCTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
ATTTTTTAAATAGAAAGGATATCATGGATTCTTTAAAGAATGAGAACTTCGACATGGTGATA  
GTTGAAACTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC  
CATTCTTTCCACTTCATTGGCTCTTTGGAATTTGGGCTACCAATCCCTTGTCTTATGTTT  
CAGTATTCGGTTCTTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG  
ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
GGTTCATTAACCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT  
GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACCTTCATTGC  
CAAGTTTGGGGACTCTGGTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGA  
ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
AAGTGTGAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGA  
CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG  
GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTT  
AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
ACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAG  
CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
TGTTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC  
TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
GGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
GCGATGTCACCATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTAGTCCTTC  
TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
TAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT  
CTTGTCTCTCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
GACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCTTCTCATGCGCCTCTCCGAA  
TCACACCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC  
TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTCTTTTCTGTTTCTGTTT  
TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAGGGC  
CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT  
TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGA AAAATAAAAGTTTACA  
CGGTTATCTCTCCCAACCTCACTAA

**FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGF  
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF  
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFGLPIPLSYVPV  
FRSLTDMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF  
INSDFAFDFAFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP  
EIFKEMNNAFAHLPQGVWKCQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ  
NSIMEAIQHGVPVMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK  
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQPWHEQYLFDFVFVLLGLT  
LGTWLWLCGKLLGMAVWWLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATAACCATGTT  
CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT  
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA  
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAACCTGCAGTGACAGCAGGAGTAAGAGT  
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGC  
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA  
AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC  
TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
GGGTGGGCCCAGGAGGGGTTCAGAGCCCGTCTGTGAGGGGGAGTGCCTGGTGGTCTGTGA  
GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
GAGTGGCATTGTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
ACCAGTGGGGCCATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
CTCTGGCTCCTTCGTAGCCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGG  
TGTACAACCGCCAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC  
TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA  
CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCCGGGGGAATCTACTGGGTGGTTGGAAATACT  
CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCACAGAAT  
CCAGCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCCTGTGCCAAACACCCCAAGTTTAA  
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTTAA  
CTCCCAGCCACCTGCTGCATCTGTTCTTCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCACCCAGCTTCCT  
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCCAG  
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTCTGTGAGGAAAGCCAGCATCACGGATC  
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC  
CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCCTCCAGCTCTC  
TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT  
CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTTATTACCTGGGATTCCATGATTATTCTT  
CAGACCTCTCCTGCCAGTATGCTAAACCCTCCCTCTCTCTTCTTATCCCGCTGTCCCATT  
GGCCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT  
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA  
TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAATTAATAA

**FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECVLVCEPGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRG  
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

164/270



**FIGURE 163**

GCTGTTTCTCTCGCGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCCTAGCCGCCCAGC  
CTCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGGCAT  
GGGCCAGGGGCGCGGGGTGAAGCGGCTTCCCGCGGGGCCGTGACTGGGCGGGCTTCAGCCAT  
GAAGACCCTCATAGCCGCCTACTCCGGGGTCTGCGCGGCGAGCGTCAGGCCGAGGCTGACC  
GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGTGCGCGGAGGGGTCTGGGAGATGGGGCACT  
GGATCCAGCATCCTCTCCGCCCTCCAGGACCTCTTCTCTGTACCTGGCTCAATAGGTCCAA  
GGTGAAAAGCAGCTACAGGTCACTCTCAGTGCTCCAGTGGGTCTGTCCTTCCTTGACTGG  
GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG  
CTCTACTTCACTTGGCTGGTGTGTTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTCACA  
GTGGGTCCGAAACTGGGCTGTGTGGCGCTACTTTGAGACTACTTTCCCATCCAGCTGGTGA  
AGACACACAACCTGCTGACCACCAGGAACCTATATCTTTGGATACCACCCCATGGTATCATG  
GGCCTGGGTGCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCAGG  
CATACGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCCTGTGTTGAGGGAGTACC  
TGATGTCTGGAGGTATCTGCCCTGTGAGCCGGGACACCATAGACTATTTGCTTTCAAAGAAT  
GGGAGTGGCAATGCTATCATCATCGTGGTCCGGGGTGCGGCTGAGTCTCTGAGCTCCATGCC  
TGGCAAGAATGCAGTCACCCTGCGGAACCGCAAGGGCTTTGTGAAACTGGCCCTGCGTCATG  
GAGCTGACCTGGTTCCCATCTACTCCTTTGGAGAGAATGAAGTGTAACAAGCAGGTGATCTTC  
GAGGAGGGCTCCTGGGGCCGATGGGTCCAGAAGAAGTTCCAGAAATACATTGGTTTCGCCCC  
ATGCATCTTCCATGGTCGAGGCCTCTTCTCCTCCGACACCTGGGGGCTGGTGCCCTACTCCA  
AGCCCATCACCACTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG  
CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA  
CAAGACCAAGTTCCGGCCTCCCGGAGACTGAGGTCTGGAGGTGAACTGAGCCAGCCTTCGGG  
GCCAATTCCCTGGAGGAACCAGCTGCAAAATCACTTTTTTGCTCTGTAAATTTGGAAGTGTCA  
TGGGTGTCTGTGGGTATTTTAAAAGAAATTATAACAATTTTGCTAAACCAAAAAAAAAAAAA  
AA  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGRRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM  
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYQVIFEESWGRWVQKKFQKYIGFA  
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK  
HKTKFGLPETEVLEVN

**Important features of the protein:**

**Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-  
245, 318-323, 378-383

**FIGURE 165**

GGGCGGCGGGATGGGGGCCGGGGCGGGCGGGCGCCGCACTCGCTGAGGCCCCGACGCAGGGCCGGGCGGGGCCCA  
GGGCCGAGGAGCGCGGGCGGCCAGAGCGGGGCCGCGAGGCGACGCCGGGGACGCCCCGCGCAGCAGCAGGTGGCG  
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGGA  
CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCGCTGCTGGCCTTCTGAAGACCCA  
GTTCTGTCTGCACCTGCTGGTTCGCTTGTCTTCTGTTGAGTGGTCTGGTTCATCAACTTCGTCCAGCTGTGCAC  
GCTGGCGCTCTGGCCGGTTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA  
ACTGGTTCATGCTGCTGGAGTGGTGGTCTGACGGAGTGTACACTGTTACGGACCAGGCCAGGTAGAGCGCTT  
TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA  
GCGCTTCGGAGTGTGGGGAGCTCCAAGGTCTCGCTAAGAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC  
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG  
GCGCTGTGCGACTACCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA  
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG  
CTTCAACCACCGCAGTCAAGTGCTCCGCGGGGACAGTCGAGCTGCTATGATGTAACCTGAACCTCAGAGGAAA  
CAAGAACCCGCTCCCTGCTGGGGATCTCTACGGGAAGAAGTACGAGGCGGACATGTGCTGAGGAGATTCTCTT  
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA  
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCGGTGGACCTCTCTGAA  
CTTCTGTCTGGGCCACCATTTCTCTGTCTCCCTCTTCAAGTTTGTCTTGGGCGCTTTTGCCAGCGGATCACC  
TCTCTGATCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCTTTGGAGTTCGCGAGCTGATAGGAGAATCGCT  
TGAACCTGGGAGGTGGAGATTGCAGTGGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT  
CAGTCTCAAAAAAAAAAAAAAAAACAAAAAAAAAACCCAGAAATCTGGAGTTGAACGTGTGTAGTTACTGACATGAAAA  
ATTCACTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT  
TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA  
CATATGCATGATGAGAGTCCAGAGGAGAGGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA  
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCAT  
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG  
ATCAGATTAACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA  
AACCTTCAACTGTAATTATTGGACTTTTGAGTCTTAGATGGTCTGACCTCTTGTCTTCAGGGACAGTTTTTCA  
ATTTAATCCCTAATAACAATTAGTCAAGCTTCCCTGACCTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGGC  
TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTGGGGTCAGGCTGATCTCAAACCTCCT  
GAGTTTCAGGTGATCTGCCGCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA  
ATTTCTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCAGCCTGTGATCCCAAGTAGCTTGGATTGTA  
AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT  
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA  
GCATCTTGTGATGTGCTTATTGGCCATTGTATATCTTCTATCTTCTTTGGGAAATGTCTGTTCAAGTCTTTG  
CCTTTTTAAATTTTTATTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT  
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT  
AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA  
TGCCCAGGCTGGTCTTGAACCTCCTGAGCTCAAGTATCTGCCTGCTCAGCCTCCCAAAGTGTGGGATTACAGA  
CATGAGCCACTGCACCTGGCAAACCTCCAAAATTCACACACACACAAAAAACCACTGATTCAAATGGGCA  
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGATGAGAAGTCGAGGCTG  
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

**FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFVVFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV  
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK  
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR  
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAYVDVTLNFRGNKNPSLLGILYGKK  
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN  
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGVGAASFGVRRRLIGESLEPGRWRLQ

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

**FIGURE 167**

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG  
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT  
ACATGTGGTGTCTCTTGTCTGTTCCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT  
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC  
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTTTAATGCTCTCATAAGACCACTTGTTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC  
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
TGCAGGTCCTGATTCAGTAGGCCCAGGTGGGCATCTCTAACAACTCCCACGTGATGCTGA  
TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

**FIGURE 168**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRHIHLVCVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR  
EGKINFYTN GDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS  
GPCPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

**FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAAAATCTGTTTTTTGTTCTCTTGTAAGTAGCCTTTACCTTCCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGTTA  
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTT  
CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
CCAGGACGGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT  
CTAACCTTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
GGGAAGGAACCTTGCGCAAATTATGGGTGAGAAAGATGGAGGTGTTGGGTTATCACAAGGC  
ATCGAGTCTCCTGCATTGAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
GCTCAGTGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAA  
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAAATTACTTGAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAAGAATTATGGTTATTTGTAA

**FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVMFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA  
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15



**FIGURE 171**

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
CCGCCGCCTCCTGCCCCGCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCGCGCT  
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT  
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCCGCGACGGGCGCGTGCTGACCTGCGAGGTGGACGCGCA  
GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC  
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC  
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGAAGGTGCTGC  
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGCCCTTCAAGAT  
CTAGGGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCCAGGAATTGAC  
CCTGAGTTTAAATTGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

**FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282

><subunit 1 of 1, 262 aa, 1 stop

><MW: 28809, pI: 8.80, NX(S/T): 1

MTQVPVRLSVPAALALGSAALGAFAFATGLFLGRRCPWPWRGRREQCLLPEDSRLWQYLLSRS  
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL  
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRLLKPALETLDELLAAGEAGTFDVAVVDA  
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS  
LLPLGDGLTLAFKI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

**FIGURE 173**

CCGCCGCCGACGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCTGGGCCTCTCGCCGTCA  
GCATGCCACACGCCTTCAAGCCCCGGGACTTGGTGTTGCTAAGATGAAGGGCTACCCCTCAC  
TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCCGTGAAGCCCCACCCAACAAGTACCC  
CATCTTTTTCTTTGGCACACACGAAACAGCCTTCCTGGGACCCAAGGACCTGTTCCCTACG  
ACAAATGTAAAGACAAGTACGGGAAGCCCAACAAGAGGAAAGGCTTCAATGAAGGGCTGTGG  
GAGATCCAGAACAACCCCCACGCCAGCTACAGCGCCCCTCCGCCAGTGAGCTCCTCCGACAG  
CGAGGCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACGATGAGGACCGGG  
GGGTCATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCTGCGCTAAAGATGTC  
GGTCTCGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG  
AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT  
GAGAAGAAAGCAGCGGTCCGGGCGCCACGGAGGGGCCCTCTGGGGGGACGGAAAAAAAGAA  
GGCGCCGTACGCCTCCGACTCCGACTCCAAGGCCGATTCGGACGGGGCCAAGCCTGAGCCGG  
TGGCCATGGCGCGGTCCGCGTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCGACTCCGATGTG  
TCTGTGAAGAAGCCTCCGAGGGGAGGAAGCCAGCGGAGAAGCCTCTCCCGAAGCCGCGAGG  
GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG  
TGGACCGCATCAGTGAGTGGAAGCGGCGGGACGAGGCGCGGAGGCGCGAGCTGGAGGCCCGG  
CGGCGCGGAGAGCAGGAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAAGGAGGAGAAGGA  
GCGGAGGCGCGAGCGGGCCGACCGCGGGGAGGCTGAGCGGGGACGCGGCGGCAGCAGCGGGG  
ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT  
CCCCCGTCTCCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC  
GAAGAAGCCGCAGTCTCAAGCACAGAGCCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG  
TGCGGCCCCGAGGAGAAGCAACAAGCCAAGCCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC  
GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGAGCCCTCCGTGGAGGAGAAGCT  
GCAGAAGCTGCACAGTGAGATCAAGTTTGCCCTAAAGGTGACAGCCCCGGACGTGAAGAGGT  
GCCTGAATGCCCTAGAGGAGCTGGGAACCTGACAGGTGACCTCTCAGATCCTCCAGAAGAAC  
ACAGACGTGGTGGCCACCTTGAAGAAGATTGCGCGTTACAAAGCGAACAAGGACGTAATGGA  
GAAGGCAGCAGAAGTCTATACCCGGCTCAAGTCGCGGGTCTCGGCCCAAAGATCGAGGCCG  
TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG  
GAGCTGGCCGGGGAGGAGGCCCCCCAGGAGAAGGCGGAGGACAAGCCCAGCACCGATCTCTC  
AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCACG  
AGGAGGGTTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC  
GTACGGGAGGGTCCCGACCTGGACAGGCCTGGGAGCGACCGGCAGGAGCGCGAGAGGGCACG  
GGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGAGCCGCGGGCAGCCAGGCCAGCCCCCGC  
CCGAGCTCAGGCTGCCCCCTCCTTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAAGTGTGGG  
GAACGCTGTGCTGTTGTATTGTTCCTTGGGTTTTTTTTTCTGCCTAATTTCTGTGATT  
TCCAACCAACATGAAATGACTATAAACGGTTTTTTAATGA

**FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD  
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRG  
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE  
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRRDEARRRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAQKPVKVERTKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEEKLAGEEELAGEEAPQEKAEDKPDSTDLAPVNGEATSQKGESAEDKEHE  
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13

**FIGURE 175**

GTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
ACACCATTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTCTTCCAGTCACTGGCACTTTGAAGCA  
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTGGGTTTCATC  
AGAAGGACTGGATTTTCAAACCTCTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT  
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTTAAAGAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA  
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAAATGTGCAATTTTCATCAGAGTACTTCAGCCCTATAACAA  
AACTCACATATATGTGTGTGGAACCTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC  
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT  
CACTCGATCCCTTGGGCCCTACTCATGACCACCACTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATGG  
AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTCG  
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGAAATGATGT  
AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG  
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT  
AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT  
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT  
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA  
TGATGTCATCAGTTTCATAAAGCGGCCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT  
CAAGAGAAATCAATGTGGAATTACAGACTGACACAGATAGTGGTGGATCATGTTCATGCAGAAGATGGCCAGTACGA  
TGTAATGTTTCTTGAACAGACATTGGAACCTGTCTCAAAGTTGTCAGCATTTCAAAGGAAAAGTGAATATGGA  
AGAGGTAGTGTGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA  
GCAACAAATGTACATTGGTTCCCGAGATGGATTAGTTAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC  
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC  
TTCTAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTGTCTGGGACATCGAAGACAG  
CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC  
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA  
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTGCGAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG  
CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCTTGAAGATGAACAGATGGA  
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA  
CTACATCCAAATCCTTAGCAGCCCAAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG  
GAGACAGAGAAACAAGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA  
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAAGTTTTCTACTTAAATTTAAAGAAAAGAAATTCCTTACC  
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG  
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTGAAACAGTTTTT  
CCAAGAACAAATCTTGACAAGCAAAGTATAAGAATTTATCTAAATAAGGGGGTTTACAGTTGTAAATGTTTTA  
TGTTTTGAGTTTTTGAATTTATTGTCTGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT  
GCTTTATCCCTCGAATGTCCATTAAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT  
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTCAGACACAAATTAAGACAACCTCCATTATC  
AACAGGAACTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTTATTTCTTTC  
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT  
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCCTTAGTTATGTGTTTTTTAGAGTATATACTAA  
GCTCTACAGGGACAGAATGCTTAATAAAATACTTTAATAAGATATGGGAAAATATTTTAAATAAACAGGAAAACA  
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT  
AAATCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA  
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACA  
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC  
AATGATATTTTCAGTATATATTTTCTCTCTTTTAAAAAATATTTATCACTCTGTATATTATTTCTTTTACTGC  
CTTTATCTCTCTGTATATTGGATTTTGTGATTATATTGAGTGAATAGGAGAAAACAATATATAACACACAGA  
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTGTTGAATAACAGAACGAGTGTAAAATTTTAAAC  
AACGGAAAGGGTTAAATTAACCTCTTGAACATCTTCACTCAACCTTTCTCATTGCTGAGTTAATCTGTTGTAATT  
GTAGTATTGTTTTTGAATTTAAACAATAAATAAGCCTGCTACATGT

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1; 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLTYKDLLLSNSCIPFL  
GSSEGLDFQTLILLDEERGRLLLGA KDHFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDI IIFKLDTHNLESGRLKCPFD  
PQQPFASVMTDEYLYSGTASDFLGKDTAFT RSLGPTHDDHYIRTDISEHYWLN GAKFIGTFF  
IPDTYNPDDDKIYFFFRE SSEQGSTSDKTILSRVGRVCKNDVGGQ RSLINKWTTFLKARLIC  
SIPGSDGADTYFDELQDIYLLPTRDERNPVVG VGVFTTTSSIFKGSAVCVYSMADIRAVFNGP  
YAHKESADHRWVQYDGRI PYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV  
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE  
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRC DTYGKACADCCLARDPYCAWDGNA  
CSRYAPTSKRRARRQDV KYGDPITQCWDIEDSISHETADEK VIFGIEFNSTFLECIPKSQQA  
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLTLN  
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN  
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

178/270

**FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGA  
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC  
CTCAGCAGTTTCAGCCAGCAGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA  
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC  
GGGTGAGGTGGGGGGGCACAGGTGTCTGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG  
AGCCATTGAGGGTGTCTGAGGCTACAGAGGGGAGGAAAGGTATTTTAAGGTAACAGTGTGGCAATAGTTAA  
GAGCACAGTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTGTGCTTCTAGTTCTGTAGCCCCAGGT  
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG  
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT  
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGGCACAGGTGAGCC  
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC  
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC  
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG  
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC  
AAGACAGTGACAATCCCTGCGGGGCAGAGCCCACAGCATTCTTGGCACAGGCCCTGTACAGCTACACCGGACAGA  
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGGCCAAGATGGAGTAGATGACG  
GCTTCTGGAGGGGAGAAATTTGGGGGCCGTGTTGGGGTCTTCCCTCCCTGCTGGTGGAGAGCTGCTTGGCCCCC  
CAGGGCCACCTGAACCTCTCTGACCCTGAACAGATGCTGCCCTCCCTTCTCCTCCAGCTTCTCCCCACCTGCAC  
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCTCTGG  
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCGGCTAAAGCCCCGGATCCTGGCCACC  
CAGATCCCCCTCACCTGAAGGCCAGGGAAGCCTTGACCCCACTGATGCTGCTGTCCCTATCTTCAAGCTGTCAGA  
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCACCTCCAAGGCT  
GGAAACTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTCCCATTTGTTCTATCATCTCTAGGACC  
GGAACCTACTACCTTCTTCTGTCTGATGACCTATCTAGGTTGGTGAAATGCCTGAAATCTCTGGGGCTGGAACCC  
ATCCATCAAGGTCTCTAGTAGTTCTGGCCCACTCTTTCACCCCTGGCTCCATGACCCACCCCACTCTGGATG  
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGCCAGGATGCAAGCAG  
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCTGGGCTCTTGTG  
CTAAGAGGGCAGGGGGCTACGGTGTCTATTGCTTTAGGGGGCCACCACGGGCAGGGGCTGCTCCAGCTGCCAC  
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC  
TGAGGGGCTGTGACCTCTCTGAGGCCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC  
AGCTGGGGGGCAGTGTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
TCCATGACCAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC  
TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGATTTATAGCAAAGGCTAAGCCTGC  
AGTTTACTCTGGGGTTTCCAGGAGCCGAAAGGCTTAAATAGTTTAAGTAGGTGATGGGAAGATGAGATTACCTCA  
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG  
TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGTGC  
AGTCCCGCTGTGTTTTCTACCTGGTGATCAGAAAGTGTCTGGTTTGCTTGGCTGCCATTGCTCTTGTAGTGG  
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCCCAGTGTGCTGCTGAGAGCTCTGGGGTTCCCTTCAAGTG  
CAGAGGGGTTAGGCTGTGTCCCTGAGTCCCTCATTTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC  
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG  
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGACGTCCATAGCGCT  
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG  
GCCCTCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCTTCTC  
AGATTGTGGGGCATTGTGTAGCCTGACTTCTGTGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCCACTT  
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCAGCTGCCCCACCTGCCCA  
CAGAGAACACAGTGGTCTCCCTGTCCGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG  
GCCTCTTGTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC  
CGTCTGTGAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTCCCT  
TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCTTAAACCCCAAGCCCCAATTTCCCAAGCCCCATTT  
TTTCTGTCTTTATCTAATAAATCAATATTAAG

**FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQEERLSEARLSQRDLSPTAEDAELS  
DFEECEETGELFEPPAPQALATRALPCPAHVVFQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGFVPERYLNFPDLSLPSSQSDSNPCGAEPFLAALYSYTGQSAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS  
FSPPAPTSVLDGPPAPVLPDGDALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT



**FIGURE 179A**

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA  
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGTCTTACAGAGGGAGAGCCAGAGAAGCTGCAGA  
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG  
GCACCTCTCCCAAGCCCCAAGGACTAAGTTTTCTCCATTTCCTTTAACGGTCTCAGCCCTTCTGAAAACCTTGCC  
TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT  
GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGCCATGTCCAGACAGGCTCGCATCCCGGGAGGGG  
CTTGGCAGGGCGCTGGCTGTGGGAGCCCCAACCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG  
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT  
CGTGTTCAGAGAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA  
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA  
CCTGGGCCAGGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGGCTGAACTCCA  
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCTACGCCGAAGAGTCC  
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCCAAGAGCCAA  
GCGCTTTGCTTCACTAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCTTCCACGGTGC  
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAAGGCCCTCAAGCACCCAAAGCATCCGCAATCC  
TGTCAGCTTGGTGGTGACTCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGCCCAAGTGGGGCCAGTGCTGC  
CCAGACCCCTCGCGAGCTTCTGTGCTTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA  
CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGGCAGACGCTGGGTATGGCTGATGTGGG  
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGTCA  
TGAAGTGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCTTTGAGCAC  
CTCTCGCCATGTGATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCTT  
CATCACTGACTTCTGGAACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT  
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCCGACTCACGCCATTGTCC  
ACAGCTCGCCCGCCCTGTGCTGCCCTCTGGTGCTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA  
CTCGCCCTGGGCGCATGGGCACACCCCTGCGGGCCCCGACAGGCCCTGCATGGGTGGTGCCTGCCATGGACCA  
GCTCCAGGACTTCAATATTCCACAGGCTGGTGCTGGGTCCTTGGGGACCATGGGGTACTGCTCTCGGACCTG  
TGGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG  
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
GTGTGCTGCCTACAACCACCGCACCGACCTTCAAGAGCTTCCCAGGGCCCATGGACTGGGTTCCTCGCTACAC  
AGGCGTGGCCCCCAGGACAGTGCAAACTCACCTGCCAGGCCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC  
ACGGTGGTAGATGGGACCCCTGTTCCCCGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG  
CTGTGATCGCATATTGGCTCCAAGAAGAAAGTTTGACAAGTGATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG  
CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGATAAGGATACAACAAATGTGGTCACTATCCCCCGGGGGCCACCCA  
CATTTCTGTCCGGCAGCAGGGAAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCTA  
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTA  
CAGCGGGGCCACTGCAGCCTCAGAGACACTGTGAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTC  
AGTGGCTGGCAACCCCCAGGACACACGCTCCGATACAGCTTCTCGTGCCCCGGCCGACCCCTTCAACGCCACG  
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG  
GAAATAACCCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT  
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT  
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCCGAGGAGGCACTGATGGGTTAGTGGATGGAAGGGGCTGACAGAC  
AGCCCTCCATCTAACTGCCCCCTCTGCCCTGCGGGTCAAGAGGGAGGGGGAAGGCAGGGAGGGCCTGGGCC  
CAGTTGTATTTATTTAGTATTTATTTCACTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA  
CCTGACCCCTGACCCCTCATAGCCCTCACCCCTGGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTG  
TGTGTATGCGTGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTC  
TTCCTGAATTTTATTTTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCTTCAGGGAGTGAGGGATTATCTTTT  
TTTTTTTCTTTCTTTCTTTTCTTTTGTGAGACAGAATCTCGCTCTGTGCGCCAGGCTGGAGTGCAATG  
GCACAATCTCGGCTCACTGCATCCTCCGCTCCCGGTTCAAGTGATTCTCATGCCTCAGCCTCCTGAGTAGCTG  
GGATTACAGGCTCCTGCCACCACGCCCAGCTAATTTTTTTGTTTTTGGAGACAGAGTCTCGCTATTGTG  
ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCGCCACCTGGGTTCCAGCAATTCTCCTGCTCAGCCTCC  
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCCGCTAATTTTTGTATTTTGTAGAGACGGGGTTTAC  
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCCAAAGTGTGGGATT  
ACAGGCGTGAGCCACCGTGCTGGCCACGCCCCAATAATTTTTGTATTTTGTAGAGACAGGGTTTCAACATGT  
TGGCCAGGCTGCTCTTGAACCTGACCTCAGGTAATCGACCTGCCTCGGCCTCCCAAAGTGTGGGATTACAGG  
TGTGAGCCACCACGCCCCGTACATATTTTTTAAATTTGAATTTACTATTTATGTGATCCTTTTGGAGTCAGACAG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCATTTGCCAATAATAATACCTCCCTTAGAAG  
TTTGTGTTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAGGAAA

**FIGURE 180**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNGLSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHLRRKSP
ASGQGPCMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGAVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPDWLHRRQAQILEILRRRPWAGRK
```

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 358-367

183/270

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT  
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTTCTTAAAAATTCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG  
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTATTGTTGTATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT  
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT  
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAAAA

**FIGURE 182**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILVLFWGSKHFVPEVPPKAY  
DMEHTFYNSGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKT  
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWWPAEKPIENRDFLKNKILEICDNVTMYWI  
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY  
TENGIEFDPMLDERGYCCIIYCRGRNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV  
ARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

185/270

**FIGURE 183**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG  
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
GCGCCTGCGCCGTTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA  
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
GGCACCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC  
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA  
ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT  
TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTTPAKTTFAILGGTL  
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYRPHYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

**FIGURE 185**

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCACACCACATGCCAAGTGGTGGCGTTCCT  
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
GTGAGGCAGAGTTTCAAGGCTTACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC  
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
AACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
GTCTGTGTTTGCCAAACATGCTGGTGACTAATTCTGGATGTCCACAGCTAACATGTACACCG  
GCATGGGTGGGATGGTGCAGACTGTTTCAAGACCAGGTACACATTTGGTGCGGCTCTGTTCGTG  
GGCTGGGTGCGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG  
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG  
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
TGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTACCCAAAA  
AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
CTCGATTTTATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC  
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
TTCTTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC  
ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA  
TTTCCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA  
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
TGATCTTAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG  
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG  
TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
TTAAGTCCTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA  
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT  
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC  
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAAGTTCGAGACTAGCCTG  
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA  
ACTAATTCTTTAA



**FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 27856, pI: 8.50, NX(S/T): 1  
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

**FIGURE 187**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG  
GAGTCCAGCTGGCTAAAACATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG  
GGCTGTTTCTTGGTGGTGTGGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGG  
AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTTGCTGG  
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC  
TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCCTGGTGCT  
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACCTTCCCATCGCACAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG  
AGCGTCTACTCCAGAAGTCAGTATGTGTAAGTTGTGTATGTTTTTTAACTTTACTATAAAGC  
CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA  
CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA  
GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTACTTCAAATGACATTGCT  
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
TCCATTACACTGAATAAATAGAAGTCAACTATTGCTTTTTCAGGGAAATCATGGATAGGGTTG  
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA  
AGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTCTGATATGCTG  
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT  
TTCTTGTGTATTAAATTAACATTTTTTAAAACGCAGATATTTTGTCAAGGGGCTTTCATTCA  
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
GTTTTAGGAAAGTGAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA  
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
AATATAAATAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGCTTACCAAAAAACAACA  
ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG  
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTACCATTCTGTTTAGTTTTACTAAA  
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAAATCCAATTTGA  
AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTTATA  
TTAATAAATTGTACATTTTTCTAATT

**FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM  
QCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGGTCTACCTTGCTGGGGC  
CAAGTGTAACCACTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTTCATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT  
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT  
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTTCTTTTGAAGTATTTAAATTCATTT  
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC  
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAGGACTGCCCACCTCCGGAATTCTGACCTCTGTTTCTCCGTCCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTACCCCTTTACTCACATTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA

**FIGURE 190**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736  
><subunit 1 of 1, 220 aa, 1 stop  
><MW: 23292, pI: 8.43, NX(S/T): 0  
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWLMSCVVQSTGQM  
QCKVYDSSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLPVCWTAHAIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP  
SGGSQGPPSHYMARYSTSAPAIISRGPPSEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATT TTTATCCC  
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCT  
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
TAGCTCCTTGTTGGCTCTCCCGCTGCCCTGGAAACAGCCGGGCCCTCATGTGTGTGGCTG  
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGCCAAAGCATACTTCTGGGAACTTCAGGAGTCTCTTCATCCTGAC  
GGGTATCTTCGTTCTGATTCGGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
ACCCAGCCATCCACATAGGT CAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT  
ATGGACTATGGTCAATGT TTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA  
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
TGTACAATGATGGACTACTTATTACTTTTGGACCATCATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

**FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737  
><subunit 1 of 1, 173 aa, 1 stop  
><MW: 18938, pI: 9.99, NX(S/T): 1  
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAGTGGAAGTGCAGCATTTCACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAATAATCTCCAGA



## **FIGURE 194**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN

ECHLCTESLKSNGRVQFLHDGSC

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGCTGCCTCCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT  
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

## FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLKMLQKREAPVPTKTKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDYYQRHYD  
EDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

**FIGURE 197**

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
CGTCCTTTTCTCGGTGCTTGCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA  
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTGAGGGACCCCAACGCCATCCCAGCCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTTACAGCAACACCGCCAG  
CCCCGGA CTCCCCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTCAGAGCAG  
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG  
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG  
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
CCAAATCCCCCTGCCCCGCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT  
GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG  
GCCTTTGCCATGTACCGCCCGTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC  
GGACCTTGCTCCCCGCGCCGCGGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCCGA  
CTGGGAGTGGGCTCCTCGGGGTGGGGCATCTGCTGTGCTGCCTCGGCCCGGGCAGAGCCG  
GGCCGCCCCGGGGGCCGTCTTAGTGTTCTGCCGAGGACCCAGCCGCCTCCAATCCCTGAC  
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG  
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA  
AAAAAAA

## **FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRLKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217



**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI

NENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNNLAGIHCAKRIVSGARGMN

NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA  
CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG  
CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC  
AATTTGAAGTCCCTGTGAATGGGCTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACGCG  
TTGGGGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACGCG  
TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA  
ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
CTGTTGCAATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
CAGACTCCAGTTCCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT  
TGCACCCTCCCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT  
GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA  
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC  
TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG  
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCTGGACCCAC  
GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG  
CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
CCAGGGCCTTCTGAAGGAGATCATCCTCGTGACGACCTCAGCCAGCAAGGACAACCTCAAG  
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
TCATGGATGCCCCTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT  
GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC  
CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
TCTTATGTCGCTGCGAGGTGGTGAAAACCTCGAAGTGTCTTTCAAGGCCTGGCTCTGTGGTG  
GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT  
TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG  
GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA  
AGCCAGACTGCATGGAACGCTTGCACTGCAAAGGAGACTGGGTGTGCGACATTCCTACTGG  
TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT  
GTCCCATGGTGTGGCTCCTTGCACTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTCAGGCAGGAGCAGGT  
GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
AGAATGGGATGATTGTCCACATTTCTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC  
AATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTTGACCA  
GATAAATGCTGTGGATGAACGATGAATGTCAATGTGCAAGGAAAAGAGAATTTTGGCCATC  
AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTATGAAGCTGATCCTTTTGTGT  
GTGTGCTCCTGTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT  
TCACACCTTATTTTATTGACTGCTGGCTGCTTA



**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEYEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPPRAFLKEIILVDDLSQQGQLKSALSEYVAR  
LEGVKLLRSNKRLLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP  
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRRLLGCRTFHWFLANVYPEL  
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCM EAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGACATGGA  
GTCCAGGATGTGGCCTGCGCTGCTGTCTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
TGCCCCCTCCACCGCCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACCAGCCCCAGCC  
CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTATGTGTGCGTGTGGGAGCGAGC  
ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCCTGCCTGGCACTG  
CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGGCCGCCCTCATCCCAATACCCCTGGGCT  
ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
ATTTCTGGACTATGGTTTTGCAGCCCCCTCATGGGCTCGCAACCCCAACCCCAACTCAGACT  
CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCTGCGGCCATTCT  
CTGTTCCGGGGCCGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT  
CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGAGAGCCAGCAGCCACTGACA  
GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACCTACCCCCACCCC  
TGACCATGAGGAGCCCCGAGGGGGACCCCGGCCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
CCTTCCAGTTGAACCGGTGAGGGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGAAGGCAAC  
TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
CTCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTTC  
CTTCTCCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCCATAACTCCAACCTCTGCCC  
TCTTTGGTTTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC  
CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCCTT  
TCCCTCTTCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC  
AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCCTTGACACACCACCCGGAACACTCCCCAGCC  
CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG  
GGTCCCTGTCCCCACCCTTGTGCACTCACATGAAAGCCTTGACACACTCACCTCCACCTTCA  
AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG  
TGGTCAGCGTTTCTGACACTTTACCTCTCATGTGCGTTTCCCGCCTGATGTTGTGGTGG  
TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC  
GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTCATGG  
TCTCGTCCCATTCCACACCATTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA  
CTGCTAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA  
AGGGACTCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTGTCTTGTCTGTCTGCTGGCTG  
TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTCCCTTCCCAGCCT  
CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC  
ATCGGGAGCTCTGCCTCCAAGTCTACCCCTCCCTTCCCGACTCCCTCCTGTCCCCTCCTTT  
CCTCCCTCCTTCTCACTGCTTTTCCACCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTCAGGTT  
CTTCCCTCCTTCTCACTGCTTTTCCACCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTCAGGCT  
GTGATATATATTTTGTATTATCTCTTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG  
GGATGTAAGTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

**FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV  
PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACC CGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA  
GGGGCCGCGCCCGGCGGCGCGACTCGGCAAAAAAAAAAAAAA

**FIGURE 206**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398

><subunit 1 of 1, 121 aa, 1 stop

><MW: 12073, pI: 4.11, NX(S/T): 0

MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG

PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGGAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGT CAGGGGCGCTGCTCACC GACTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACC GGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCCTAAGTAGCCC  
CCAGAGGCGCTGGGAGTGTGTCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT  
CGACTGT CAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG  
ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGCTCCCCGCTTCCAC  
CTGGCTGT CATCGGGTAGGGCGGGGCGGTGGGTT CAGGGGCGCACCATTCCAAGCCTGTGT  
CCCACAGGTCTCGGCGCAGTGAAGTCAGCTGTCCAGGGCCTCCTGA ACTACATAAATAAC  
TGGCACAAGTAAGTCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCTTAGAGGGGCTCCCGA  
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC  
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCACATTGCCTTT CAGACAGGACACGAGCATGAGGTAAGGCCGC  
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC  
ACGAGGGTGTCTGTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGACAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK

ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER

HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

**FIGURE 209**

AGCAGGAGCAGGAGAGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT  
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC  
ACTGAGGTGGCTGTTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
TAGCATGGTGCAAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCCTGGTAGACAATGAACAACCTG  
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
CAACAGCCTCCACATGGTGACAGAGTACAACCTGTGACTGTGATTGGGTATTCAACAGCG  
TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAATAAAGGAGTCTCAACTGCCAG  
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC  
GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAATAATGTTGAAAGAAAATCG  
TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACCTACATATGGCC  
AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG  
GATCACTAGGCCTGCCAACCACACACACACGACGTCACACACGACGACGACGCGTGCACAC  
ACACACGCGCACACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC  
TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCAAT  
CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
CCTCTATGAAAGAGAGGCATTCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT  
TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTCTTTTAAGGTTACCTAAGGGT  
TGAAACTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG  
ATGGTTTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC  
CCTGAACTCAGCAGAAATAGACCATGTGAAACTCCATGCTTGGTTAGCATCTCCAACCTCCC  
TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA



**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401  
><subunit 1 of 1, 273 aa, 1 stop  
><MW: 30480, pI: 4.60, NX(S/T): 1  
MEAAPSRFMFLFLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPVSGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGAGGTGCCACCCGGCGCGGGTG  
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
GACGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGG  
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGGCGGCGCTTGG  
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTCCACTACTC  
CCAAGGGCAAGTGTACCTTGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
CTGTGGTCTTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC  
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC  
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTCATGA  
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTTGTACTTTCTTTTC  
AGGTCATTTACAATTGGGAGATTTTCAGAAACATTCTTTTACCATCATTTAGAAATGGTTTG  
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
GGCTTAAGACTGATTAGTCTTAGCATTCTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA  
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
AAAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
AAATGTGTCAATCAATTTCTGGATTCAATAAGCAAGATTAGCAAAGGATAAATGCCGAAG  
GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAAGTAGAAAATCCAAGCTTTGCTT  
GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

**FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510  
><subunit 1 of 1, 269 aa, 1 stop  
><MW: 29082, pI: 9.02, NX(S/T): 3  
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG  
GHHSDKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCCGGGCTGCCGCC  
CCCCGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC  
TCTCGGCCACGGCTGGGTCTGGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
TGGCAGGTGGGCTGAGGGGCGCGCCCCGGCGCAGTCCCCCGCGGCCCCGACCCTGAGGCG  
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGAAAAGAAGTC  
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT  
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAA  
TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG  
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT  
ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA  
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT  
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
CAGTGATTTACAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC  
TTAACACTATTTTATTAATTAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA  
TGTTTATAAAGTAAAAAAA

**FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522  
><subunit 1 of 1, 373 aa, 1 stop  
><MW: 41221, pI: 8.54, NX(S/T): 0  
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMMLTTVQEENEPVIYNRR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT  
GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
GGAACCAGCAGGATGGTACCTTGTCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
TGGAGTCGCACCTGTCCGACCAGCTGACCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCCTGTTCTTCATGATGTCAGG  
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG  
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTTCAGAAACCCAAG  
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529  
><subunit 1 of 1, 269 aa, 1 stop  
><MW: 28004, pI: 5.80, NX(S/T): 1  
MAAASAGATRLLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRPGALDGLEA  
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ  
LQPPTTAPGPETA AFIERLEMEQAQKAKNPQE QKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGGSGLCCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGAGCAGGTCGTCCGGGGGGCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA  
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
TGGCCTTGCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
GCAAGAATTCTTGTGTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAA  
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTCTGGACCGCCGC  
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT  
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTTCATGTTGACTTT  
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT  
TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA  
GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
CCTTGCTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCACTTTGCTCTG  
CTGTATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCACCGTGGTAAGGCATGATGCT  
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TA**ACCCCACTCCAG  
GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT  
GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA  
ATAAACACTTTTAAATGATCAAAAAAAAAA



**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAIPLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPMSFLRRKVIPET  
EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFISCSAVMMALLAVVGLFTVVRHDA  
ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

**FIGURE 219**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATG  
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA  
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA  
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC  
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
TGGTAGAAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCTCACTGACTTTTTTAGCAATAAA  
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ

IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF

YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAAGTTGCACTGCTGTGTGGGCTGGTGGTGA  
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT  
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC  
CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

**FIGURE 222**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538

><subunit 1 of 1, 116 aa, 1 stop

><MW: 12910, pI: 6.41, NX(S/T): 1

MELALLCGLVVMAGVPIPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW  
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDESE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTAGCACCACCTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACTCACCCGTGGGTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

**FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK  
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFAFQAFLRGMVMYTSKDRYFYFGKLDGQISS  
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

**Signal peptide:**

amino acids 1-22

**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
GAACTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT  
TTTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATAT  
CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
TATTTGTTCTTGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
CCAAGGGGTCCAATTTTTCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG  
ACAGGGGCTGTTCATGCAACTGGCCCCAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAA  
CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTA  
TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAAGTAAAGTATAAT  
CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCC  
TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT  
ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT  
TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGTATAG  
GACAGACCATGTCTGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC  
GAAGCTTTCAGTGGACCCAGTGTTCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA  
TTCCAACAAGCTCACATTTATTTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA  
TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGTGGCTG  
AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT  
TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCAT  
GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
TGCTCGTCATCCTGTGTTATCTACGTGTCTGGAAGCGGTACCCTGCGAGCATGAAGCAG  
CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAAT  
GACTCCAGCACCCAGGAATTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA  
TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC  
TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCCTCCCCTCTCCCTCTCACTTTGGTG  
CAAGATCCTTCTTGTCCGTTTTAGTGCAATCATAATACTGGTCATTTTCTCTCATAcata  
ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGTCCGGTTAATATAA  
TACCTATTGTATAAGACCTTTACTGATTCCATTAATGTGCGATTTGTTTTAAGATAAACT  
TCTTTCATAGGTAAAAA



**FIGURE 226**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPCGCRCEGKMVYCESQKLQEIPSSISAG  
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF  
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIQDCRNLELL  
DLGYNRIRSLARNVFAFMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNLKISVIGQTM  
SWTWSSLQRLDLGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIQEILDSWISLNDISLA  
GNIWECSRNICSLVNWLSFKGLRENTIICASPKELOGVNVIDAVKNYSICGKSTTERFDLA  
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAHEHISFHKI IAGSVALFLSVLVI  
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTTETSEMLLN  
GTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
TAAATATGTCAAGATCCAGACTTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTGTTGGAGACTTGGACTCTATTTATGG  
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
ATCCTGTTCTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
AAAACAACCTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA  
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
GAAAAGTTTGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGAGCCTCAGGGCTTG  
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT  
AAACATCAATAGATATCTAAAAA

**FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA

ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP

VPAPCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA  
GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCC  
ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAACT  
CCCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTCAAGTCTTGATTTGTGGC  
TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGCTTCTTCAGAAATGTTTTTTA  
CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT  
TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
ACACAGTGGATGTGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
GCTGTCCTTCTGGATGACATTTTGAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTC  
TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC  
TCTAATTCTGTACATAAAAAATTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG  
CTGTACTATGTCCTTAAAGAGAATTTGGTAAGTGGTTGATGTGGTAAGCAGATAGGTGAGT  
TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTC  
ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGACAAGTGAAGAATGTTTAA  
TCATTCTGTCATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTG  
CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA  
AGGTTAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG  
CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT  
GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA  
AAGTATTCATGATTTTTTACATACATGAATGTTTCATTTAAAAGTTTAAATCCTTTGAGTGTCT  
ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC  
TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA  
GGTACTTTTGTGCTGCATTAAATTGCTTGGAAGTGTTAACATTATATTATATAAGAGTATC  
CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
TTAAAATAAGAACATTTAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT  
GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT  
TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT  
CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA  
TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTTCTCTCTCTGTA  
CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

## **FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
CATGCCCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAACCCGGCCATGCT  
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG  
GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA  
CTTGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT  
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTGCTCC  
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG  
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
CACAACCTCATTACCCGCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCACCAT  
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTATTGGTCCGGGTGCCTTCGCGGGG  
CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCCAG  
TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCTTGACCTGTGCGGCAACCCCAAGCTTAACT  
GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
AACCTGGTGGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCCTGGCT  
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGGCCCCACC  
ATCTTGTGA~~CA~~AAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCTCTGGGCTGCCTCAG  
GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAGTGGGGAGCCCGCAGGCCTATGTGGCA  
GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
AACCAGACTCGGGTCCCCTCCTGCTTCCCCTCCCCACTTATCCCCAAGTGCCTTCCCTCAT  
GCCTGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
GTTCAGGTCCACTGGGCTGAGTGTCCCCTTGGGCCCAGTGGCCAGTCACTCAGGGGCGAGTT  
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTCTAT  
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCTTCTCATGTGAC  
AGATGGGGAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCCGACCCAATGCACTTTCTTGTCTCCTCTA  
ATAAGCCCCACCCTCCCCGCCTGGGCTCCCCTTGCTGCCCTTGCTGTTCCTGTTCCCCATTAGCACA  
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCCAGCATCCAGACTGGAAACCTACC  
CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTAGTCCCCACTGGCCCTGAGCACGACAGC  
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCCGACCCATGTCTATGC  
TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCCTTAGTCTTCATTTTA  
TAAAAGTTGTTGCCTTTTAAACGGAGTGTCACCTTTCAACCGGCCTCCCCTACCCCTGCTGGC  
CGGGGATGGAGACATGTCAATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAAT  
ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC  
CCATCATCTATCTAACCGGTCTTGATTTAATAAACACTATAAAAGGTTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652  
><subunit 1 of 1, 353 aa, 1 stop  
><MW: 37847, pI: 6.80, NX(S/T): 2  
MPWPLLLLLLAVSGAQTRPCFPGCQCEVETFGFLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH  
LDLSSNRLEMVNESVLGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP  
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI  
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS  
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV  
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG  
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC  
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC  
TCTAGTCTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC  
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTC  
TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT  
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT  
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGGCTATTTAATGTATTT  
ATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
AGCAGGTGATGTATTTTATACAGTAAAAAAAAAACCTTGTAATTCTAGAAGAGTGGCT  
AGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT  
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
CTTCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
CCAAAAAAAAAAAAAAAAAAAA



**FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 261 aa, 1 stop

><MW: 29667, pI: 8.76, NX(S/T): 0

MRQFPKTSFDISPMSFSIYSLOVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP  
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLRLLYLDRVFKNYQTP  
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG  
ELDILLQWMEETE

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG  
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCG  
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGACA  
GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG  
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTATTGGCCAGTTTTTAGCCAATCCAAGTACCTAGTGAAGGTTGAGATGCAAAT  
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGATTTTCGTGGTGTACATCATGATTTG  
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT  
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT  
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
TTTTAA

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568  
><subunit 1 of 1, 323 aa, 1 stop  
><MW: 36064, pI: 9.33, NX(S/T): 1  
MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA  
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEH  
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTTACAGGC  
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC  
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
TTCATTGGTTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTTGGTGC  
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAAATGCACTTA  
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
TTCTTAAGTCACATTTTCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT  
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTTCATTGCATAGACTGTTAATATGTA  
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA  
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCAATTTTAGAAGTAACCACTCTTGT  
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG  
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT  
AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
TGCACTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA  
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC  
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAAVVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

**FIGURE 239**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
CTGGCGGCCCCGCAACACTCCGTCTCACCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT  
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT  
GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG  
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
TGTTTATTCTGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
GCCTCGCCCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC  
AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCACTGGTGCTGGTGG  
CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG  
GGGAGTTCCTACGCAAAACAACCTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
CCTCAGGGGTAAAAGCCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG  
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC  
TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCCG  
GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGCTGCGTGGAAGGTGCTGCAGGTCTTGCACGC  
TGTGTGCGCCTCTCCTCCTCGGAAACAGAACCTCCCACAGCACATCCTACCCGGAAGACC  
AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTGAGGG  
ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA  
TTTTTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC  
TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCCTCTAGTCCTCAAATTTCCAGTCCC  
CTGCACCCCTTCTCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC  
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA  
GCCTCTTACCCTGAGTGTGGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT  
GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCCTTACCCTGTATCTG  
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT  
GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
GAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA  
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
CCTTCTCCTGGCTGTTTATTTTATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA  
AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATTAAATTCCCTTCTCAGATACCA  
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG  
GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG  
GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTCCCTAGATA  
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA  
TATTTGGAAATTAAAGTTTCTGACTTT



**FIGURE 242**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPA SYPECGNNAQSPIDIQTDSVTFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEOLEKLQGT
L
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 243**

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC  
GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGG  
ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTC  
CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG  
ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG  
AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC  
TGCACCCACATGTGTTACCAATTTTGTGTCACACAACCTTGAGCCCAGGGCACTATCCTAAGC  
TCAGAGGAATTGCCACAAATCTTCAGGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCAT  
CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG  
GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCAGCAGGCCGCCTCCCAACTCCAGTGGC  
ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA  
GGAAGCCACCACAGAATCAGCAAATGGAATTGAGTAAGCTGTTTCAAATTTTTTCAACTAAG  
CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTGATTATATTATGGAATAGATTGA  
GACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATTTACCTGAAAATATTCTTGAAATT  
TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATTCAATGGATAAAT  
CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTTAAACATATTTGGAAA  
ACTGGAAA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLSSSE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:  
amino acids 1-16

**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCG  
GCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCC  
TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTG  
GGATCCCAGGTCCGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG  
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGCTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAA  
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAATA  
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
CCAAAGTGATTTTCACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT  
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTCTCTTAGTATAGCATTTTTAAAAAATA  
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT  
AAAAATTATTTCCAACA

**FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 247A**

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 15 = 33.3%

**FIGURE 247B**

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

251/270

**FIGURE 247C**

PRO-DNA	NNNNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%



**FIGURE 247D**

PRO-DNA	NNNNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLTVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

4 divided by 12 = 33.3 %

**FIGURE 248A**

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

int
/* _day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
/* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
/* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
/* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ {_M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
/* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

```

**FIGURE 248B**

```

/*
*/
#include <stdio.h>
#include <ctype.h>

#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
#define DINS1       1       /* penalty per base */
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
    short          n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
    int            score;      /* score at last jmp */
    long           offset;     /* offset of prev block */
    short          jmp;        /* current jmp index */
    struct jmp     jp;         /* list of jmps */
};

struct path {
    int            spc;        /* number of leading spaces */
    short          n[JMPS];    /* size of jmp (gap) */
    int            x[JMPS];    /* loc of jmp (last elem before gap) */
};

char              *ofile;      /* output file name */
char              *namex[2];   /* seq names: getseqs() */
char              *prog;       /* prog name for err msgs */
char              *seqx[2];    /* seqs: getseqs() */
int               dmax;        /* best diag: nw() */
int               dmax0;       /* final diag */
int               dna;         /* set if dna: main() */
int               endgaps;     /* set if penalizing end gaps */
int               gapx, gapy;   /* total gaps in seqs */
int               len0, len1;   /* seq lens */
int               ngapx, ngapy; /* total size of gaps */
int               smax;        /* max score: nw() */
int               *xbm;        /* bitmap for matching */
long              offset;      /* current offset in jmp file */
struct            diag         /* holds diagonals */
struct            path         /* holds path for seqs */
    *dx;
    pp[2];

char              *calloc(), *malloc(), *index(), *strcpy();
char              *getseq(), *g_calloc();

```

**FIGURE 248C**

```

/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 * where file1 and file2 are two dna or two protein sequences.
 * The sequences can be in upper- or lower-case and may contain ambiguity
 * Any lines beginning with ';', '>' or '<' are ignored
 * Max file length is 65535 (limited by unsigned short x in the jmp struct)
 * A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 * Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
    int      ac;
    char     *av[];
{
    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0;
    ofile = "align.out";
    /* 1 to penalize endgaps */
    /* output file */

    nw();
    readjumps();
    print();
    /* fill in the matrix, get the possible jumps */
    /* get the actual jumps */
    /* print stats, alignment */

    cleanup();
    /* unlink any tmp files */
}

```

main

**FIGURE 248D**

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
{
    char          *px, *py;          /* seqs and ptrs */
    int            *ndely, *dely;     /* keep track of dely */
    int            ndelx, delx;       /* keep track of delx */
    int            *tmp;              /* for swapping row0, row1 */
    int            mis;               /* score for each type */
    int            ins0, ins1;        /* insertion penalties */
    register       id;                /* diagonal index */
    register       ij;               /* jmp index */
    register       *col0, *col1;      /* score for curr, last row */
    register       xx, yy;            /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
     */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
         */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```

nw

**FIGURE 248E**

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongoing del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongoing del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */
}

```

**FIGURE 248F**

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
else if (delx >= dely[yy]) {
    coll[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
    }
} else {
    coll[yy] = dely[yy];
    ij = dx[id].ijmp;

    if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
        dx[id].jp.n[ij] = -ndely[yy];
        dx[id].jp.x[ij] = xx;
        dx[id].score = dely[yy];
    }
}
if (xx == len0 && yy < len1) {
    /* last col
    */
    if (endgaps)
        coll[yy] -= ins0+ins1*(len1-yy);
    if (coll[yy] > smax) {
        smax = coll[yy];
        dmax = id;
    }
}
}
if (endgaps && xx < len0)
    coll[yy-1] -= ins0+ins1*(len0-xx);
if (coll[yy-1] > smax) {
    smax = coll[yy-1];
    dmax = id;
}
tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)coll);
}

```

259/270

**FIGURE 248G**

```

/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC 3
#define P_LINE 256 /* maximum output line */
#define P_SPC 3 /* space between name or num and seq */

extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

print



**FIGURE 248H**

```

/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
    int    lx, ly;                /* "core" (minus endgaps) */
    int    firstgap, lastgap;     /* leading trailing overlap */
{
    int    nm, i0, i1, siz0, siz1;
    char    outx[32];
    double    pct;
    register    n0, n1;
    register char    *p0, *p1;

    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A'] & xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
}

```

getmat

261/270

**FIGURE 248I**

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapx, (dna)? "base":"residue", (ngapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);
}

fprintf(fx, ", gaps in second sequence: %d", gapy);
if (gapy) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapy, (dna)? "base":"residue", (ngapy == 1)? "" : "s");
    fprintf(fx, "%s", outx);
}

if (dna)
    fprintf(fx,
        "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
        smax, DMAT, DMIS, DINS0, DINS1);
else
    fprintf(fx,
        "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
        smax, PINS0, PINS1);

if (endgaps)
    fprintf(fx,
        "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
        firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
        lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
else
    fprintf(fx, "< endgaps not penalized\n");
}

static nm; /* matches in core -- for checking */
static lmax; /* lengths of stripped file names */
static ij[2]; /* jmp index for a path */
static nc[2]; /* number at start of current line */
static ni[2]; /* current elem number -- for gapping */
static siz[2];
static char *ps[2]; /* ptr to current element */
static char *po[2]; /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int nn; /* char count */
    int more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        rn = stripname(name[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr\_align

**FIGURE 248J**

```

for (nn = nm = 0, more = 1; more;) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;

        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
        }
        else { /* we're putting a seq element
                */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;

            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i] + +];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i] + +];
            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;

    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';
}

```

...pr\_align

dumpblock

**FIGURE 248K**

...dumpblock

```

(void) putc('\n', fx);
for (i = 0; i < 2; i++) {
    if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
        if (i == 0)
            nums(i);
        if (i == 0 && *out[1])
            stars();
        putline(i);
        if (i == 0 && *out[1])
            fprintf(fx, star);
        if (i == 1)
            nums(i);
    }
}

```

```

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)

```

nums

```

{
    int      ix;      /* index in out[] holding seq line */

    char      nline[P_LINE];
    register  i, j;
    register char *pn, *px, *py;

    for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j%10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

```

```

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
    int      ix;
{

```

putline

264/270

**FIGURE 248L**

```

int          i;
register char *px;

for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
    (void) putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void) putc(' ', fx);

/* these count from 1:
 * ni[] is current element (from 1)
 * nc[] is number at start of current line
 */
for (px = out[ix]; *px; px++)
    (void) putc(*px&0x7F, fx);
(void) putc('\n', fx);
}

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
{
    int          i;
    register char *p0, *p1, cx, *px;

    if (!(*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
        return;
    px = star;
    for (i = lmax+P_SPC; i; i--)
        *px++ = ' ';

    for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
        if (isalpha(*p0) && isalpha(*p1)) {
            if (xbm[*p0-'A']&xbm[*p1-'A']) {
                cx = '*';
                nm++;
            }
            else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                cx = '.';
            else
                cx = ' ';
        }
        else
            cx = ' ';
        *px++ = cx;
    }
    *px++ = '\n';
    *px = '\0';
}

```

...putline

stars

**FIGURE 248M**

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
{
    char    *pn;    /* file name (may be path) */
    register char    *px, *py;

    py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
    if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
```

stripname

**FIGURE 248N**

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_malloc() -- calloc() with error checkin
 * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";      /* tmp file for jumps */
FILE    *fj;

int      cleanup();                      /* cleanup tmp file */
long     lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)
    int    i;
{
    if (fj)
        (void) unlink(jname);
    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
getseq(file, len)
    char    *file;      /* file name */
    int     *len;       /* seq len */
{
    char    line[1024], *pseq;
    register char    *px, *py;
    int     natgc, tlen;
    FILE    *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

cleanup

getseq

**FIGURE 2480**

```

py = pseq + 4;
*len = tlen;
rewind(fp);

while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

char *
g_calloc(msg, nx, sz)
char *msg;          /* program, calling routine */
int nx, sz;          /* number and size of elements */
{
    char *px, *calloc0;

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
        while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

```

...getseq

g\_calloc

readjmps



**FIGURE 248P**

...readjumps

```

    if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
    }
    else
        break;
}
if (i >= JMPS) {
    fprintf(stderr, "%s: too many gaps in alignment\n", prog);
    cleanup(1);
}
if (j >= 0) {
    siz = dx[dmax].jp.n[j];
    xx = dx[dmax].jp.x[j];
    dmax += siz;
    if (siz < 0) { /* gap in second seq */
        pp[1].n[i1] = -siz;
        xx += siz;

        /* id = xx - yy + len1 - 1
        */
        pp[1].x[i1] = xx - dmax + len1 - 1;
        gapy++;
        ngapy -= siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
        i1++;
    }
    else if (siz > 0) { /* gap in first seq */
        pp[0].n[i0] = siz;
        pp[0].x[i0] = xx;
        gapx++;
        ngapx += siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
        i0++;
    }
}
else
    break;
}

/* reverse the order of jumps
*/
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
}

```

269/270

**FIGURE 248Q**

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejumps(ix)
{
    int      ix;
    char     *mktemp();

    if (!fj) {
        if (mktemp(jname) < 0) {
            fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
            cleanup(1);
        }
        if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
    }
    (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
    (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}

```

**writejumps**